Copyright

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Title:
Perfect score:
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Listing first 45 summaries
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                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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SUMMARIES
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AAR58598	AAR58859	AAY51232	AAW06827	AAR80558	AAR39703	AAP70843	AAW18228	AA014442	g
Newcastle disease	Newcastle Disease	Newcastle disease	Newcastle disease	Newcastle's diseas	Haemagglutinin-neu	Sequence of Newcas	Paramyxovirus haem	Protein of Newcast	Description

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T, Babu YS,	RES HOSPITAL.						n-neuraminidase; HN; x-ra ntiinflammatory; virucide; niratory disease; Newcast	Virus Haemagglutinin-Neuraminida			577 AA.	ALIGNMENTS	AAW10690 AAY21982 AAB36038 AAW58182 AAP96147 AAR06329 AAW44940 AAW03551 AAW03325 AAW499683 AAW18229 ABW18229 ABW97637 AAR06023 AAW97637 AAR06023 AAW97537 AAB947507 ABB94267 ABW97457 ABB94266 AAW97457 AAB9429284 AAW97457	
Rowland RS;							x-ray crystallography; ide; infection; croup; astle disease virus; NDV.	n-Neuraminidase.				d	Newcastle disease Seq ID No: 13 of U Protein encoded by Protein of Newcastle disease Newcastle di	•

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such structures to solve the structure of paramyxovirus HN homologues, mutants, co-complexes, and other crystal forms and the use of such structures, their homologues, mutants, co-complexes, and other crystal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying paramyxovirus heamagglutinin neuraminidase (HN) inhibitor useful for treating or preventing croup, by applying three-dimensional structure of active site of paramyxovirus HN to design or select inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibitor
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                  YCLSIAEISNTLFGEFRIVPLLVEILKNDGVREARSG
                                                                                   NHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKT
                                                                                                                                                   FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR
                                                                                                                                                                                                                PGRPGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY
                                                                                                                                                                                                                                                                                 GVGGGSFIDGRVWFSVYGGLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYK
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                                                                NHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKT
                                                                                                                                FSPALLYPMTVSNKTATLHSPYTFNAFTRPGS I PCQASARCPNSCVTGVYTDPYPL I FYR
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Pred. No. 5.5e-283;
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RESULT 2 AAW18228 ID AAW1

AAW18228

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Matches 575;
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                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Page 30; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crystallisation of viral attachment protein - by cleaving protein from a virosome and producing crystals by hanging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT71745
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Protein
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SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYP
                                        SATHYCYTHNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSV 240
                                                                              SGWGAPIHDPDFIGGIGKELVVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDM
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99.7%;
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Pred. No. 1.7e-282;
1; Mismatches 1;
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    Query Match
                                                                                     An artificial polynucleotide encoding an HN and/or F polypeptide of Newcastle Disease Virus (NDV) DNA, a bioprecursor of the polypeptide, or an epitopic portion of the polypeptide or an artificial nucleotide complementary to the polynucleotide are claimed. The polynucleotides are useful for preparing a probe for extracting similar genes from a gene library or for identifying the prescence of NDV virons in a sample obtd. from poultry. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                         Newcastle disease virus gene clones - comprise polynucleotide(s) encoding the HN and/or F protein of Newcastle disease virus RNA \,
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                                                                                                                                                                                                                                                                                              Example; pages 11-16;
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18-DEC-1985;
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03-APR-1991
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Matches 574; Conservative
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WPI; 1993-243210/30
                                                           Cochran MD,
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Matches 559
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             YCLSIAEISNTLFGEFRIVPLLVEILKNDGVREARSG
                                                                             NHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKT
                                                                                                                                                                                             PGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY
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                                                          NHTLRGVFGTMLDGEQARLNPASAVFDSTSRSRITRVSSSSIKAAYTT
                                                                                                                    FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR
                                                                                                                                                FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR
                                                                                                                                                                             PGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY
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Pred. No. 2.2e
8; Mismatches
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2.2e-275;
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Matches 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant swinepox viruses - having foreign DNA inserted into a site which is non-essential for viral replication, used for
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                       SATHYCYTHNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSV
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96.9%;
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Pred. No. 2.2e-275;
8; Mismatches 10;
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Recombinant turkey herpes virus (rTH) which comprise a foreign DNA sequence encoding a cytokine inserted into a XhoI site within an EcoRI #9 genomic fragment, where the cytokine can be expressed in host cells infected with the virus can be used in vaccines to protect turkeys against avian viruses. The recombinant viruses can be used for immunising birds against infectious bronchitis virus (IBV), infectious bursal disease virus (IBV), Marek's disease virus (MDV) infectious laryngotracheitis virus (IIV) and Newcastle disease
                                                                                                                                                                                                                                                                                                                                                                                                          Turkey herpes Virus; recombinant virus; vaccine; prophylaxis; immunisation; avian virus; infectious bronchitis virus; infectious bursal disease virus; Newcastle disease virus; Marek's disease virus; infectious laryngotracheitis virus; IBIDU; NDU; MDV; ILV.
                                                                                                             Disclosure;
                                                                                                                                               Recombinant turkey herpes viruses cytokine - useful in vaccines to I
                                                                                                                                                                                                                                                                                                            09-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                  Newcastle disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Newcastle disease virus haemagglutinin
                                                                                                                                     virus and other avian viruses.
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                                                                                                            Page 175-176; 249pp;
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94US-0288065
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against
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virus (NDV). They may also be used in multivalent vaccines to protect against two or more of these avian viruses. This seque is the haemagglutninin protein of the Newcastle disease virus, antigen which can be used in the recombinant vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                         FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR
                                                                                                                                                       PGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY
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            YCLSIAEISNTLFGEFRIVPLLVEILKNDGVREARSG
                                               NHTLRGVFGTMLDGEQARLNPASAVFDSTSRSRITRVSSSSIKAAYTTSTCFKVVKTNKT
                                                                                                                                       PGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY
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                                                                                                                                                                                                                                                       SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYP
                                                                                                                                                                                                                                                                                                                                     SGWGAPIHDPDYIGGIGKELIVDDASDYTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDM
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                                                                                           FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR
YCLSIAEISNTLFGEFRIVPLLVEILKDDGVREARSG
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96.9%;
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Pred. No. 2.2e-275;
8; Mismatches 10;
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RESULT 7
AAY51232
17-JUN-1999;
                                                          Avian-paramyxovirus; respiratory disease; local immunity.
                                                                                                                                     AAY51232 standard; Protein;
                             WO9966045-A1
                                           Newcastle disease
                                                                                         Newcastle
                                                                                                                       AAY51232;
                                                                                         disease
                                                                                                       (first entry)
99WO-NL00377.
                                                                                        virus LaSota
                                             virus
                                                                 gastrointestinal
                                                                        infection; lentogenic; F protein;
                                                                                                                                      577
                                                                                        genome
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                                                                 disease; poultry
                                                                                        encoded
                                                                                        protein
                                                                 pathogen;
                                                                          vaccine;
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e, 45

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without the addition of exogenous proteolytic activity. Also it is
possible to generate a stable transfected cell line that expresses the
wild-type F protein in the virus envelope therefore providing infectious
particles, useful in the form of a vaccine, especially against
crespiratory and/or gastrointestinal diseases. NDV can be easily cultured
to very high titers in embryonated eggs. Mass culture of embryonated
eggs is relatively cheap. NDV vaccines are relatively stable and can be
simply administered by mass application methods e.g. drinking water or
by spraying or by aerosol formation. The natural route of infection is
the respiratory and/or gastrointestinal tract which are also the major
routes of infection of many other poultry pathogens. NDV can induce local
immunity despite the presence of circulating maternal antibody. This
sequence represents a protein encoded by the NDV strain LaSota genome
which is described in the method of the invention.
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Best Local Sim
Matches 560;
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60; *Conservative
                                                                                                                                                                                                                                                                                                                                                     GVGGGSFIDGRVWFSVYGGLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYK 360
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                                                                                                  FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR 480
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NHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKT 540
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97.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2920; DB 21;
Pred. No. 2.2e-275;
8; Mismatches 9;
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RESULT 8
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ID AARS9859
ID AARS9859
ID AARS9859
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                                                                                                                                                                                                                                                                                                                                                                                       Newcastle Disease Virus (NDV) HN and F genes were inserted as a Sfil fragment into the homology vector 443-88.8 at the unique Sfil fragment into the homology vector 443-88.8 at the unique Sfil site. The NDV HN and F genes were inserted in the same transcriptional orientation as the ORF in the parental homology vector. The sequence of Sfil fragment is in AAQ6894J/R58858/AAR58859.

The inserted Sfil fragment has the following structure: Junction A - Fragment 1 (HN, AAS 2-577) - Junction B - Fragment 2 (FR.322) - Junction D.

Fragment 1 is approx. 1811 bp AvaII to NacI fragment of the NDV HN CDNA clone (B1 strain). Fragment 2 is an approx 1812 bp BamHI to PstI fragment of the full length NDV FCDNA (B1 Strain). Fragment 3 is an approx 235 bp PstI and ScaI fragment of the plasmid PBR322.

The sequences of the Junctions are in AAQ68945, AAQ68946, AAQ68947 and AAQ68948.
                                                                                                                                                                                                                          Query Match
Best Local 9
                                                                                                                                                                                                  Matches 558;
                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant fowl pox virus for use in vaccines - genes expressing antigens of Newcastle disease virus infectious bronchitis virus
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N-PSDB; AAQ68943.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Newcastle Disease Virus HN gene product
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13-APR-1995
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(SYTR )
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SYNTRO
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RISRAEEKITSALGSNQDVVDRIYKQVALESPLALLNTETTIMMAITSLSYQINGAANNS
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                                                                                       DRAVSQVALENDEREAKNTWRLIFRIAILFLTVVTLAISVASLLYSMGASTPSDLVGIPT
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                                                                                                                                                                                                  Conservative
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(first entry)
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96.9%;
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                                                                                                                                                                                                  Score 2915; DB 15;
Pred. No. 7e-275;
8; Mismatches 10;
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ARESULT 9
AARS58598
AD AARS
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XX AARS
XX Newc
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XX Newc
XX Synt
XX Synt
XX W094
PN W094
PP 28-I
XX C8-I
XX WPI
DR WPI
XX New
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 AAQ70570 is the SfiI fragment insert in contg. Newcastle disease virus (NDV) HN
                                                             New recombinant fowl pox viruses - useful as vaccines against fowl pox virus, Newcastle Disease Virus and infectious laryngotracheitis virus.
                                                                                                                  WPI; 1994-294008/36.
N-PSDB; AAQ70570.
                                                                                                                                                                                                           26-FEB-1993;
                                                                                                                                                                                                                                                              01-SEP-1994.
                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                        Newcastle disease virus; HN
                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR58598
                                       Disclosure;
                                                                                                                                                                                                                                    28-FEB-1994;
                                                                                                                                                                                                                                                                                      WO9419015-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTLRGVFGTMLDGEQARLNPASAVFDSTSRSRITRVSSSSIKAAYTTSTCFKVVKTNKTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATHYCYTHNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSVS
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                                     Page 77-79; 97pp; English.
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                                                                                                                                                                                                           93US-0024156
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                                                                                                                                                                                                                                                                                                                                      gene;
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Homology Vector 502-26.22 and F genes. The structure
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RESULT 10
AAW10690
ID AAW11
XX
AC AAW11
XX
DT 05-MJ
XX
Powlg
KW Fowlg
KW immur
KW poult
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Newca
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Best Local S
Matches 558
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- Junction B - Fragment 2 (NDV F AAS 1-553) - Junction C - Fragment
3 (pBR322) - Junction D - 3'. Fragment 1 is AvaII to NaeI fragment
of the full length NDV HN cDNA clone (B1 strain). Fragment 2 is
BamHI to PstI fragment of the full length NDV F cDNA (B1 strain).
Fragment 3 is a PstI and ScaI fragment of pBR322. The structures
of the Junctions A, B, C and D are given in AAQ70552, AAQ70553,
AAQ70554 and AAQ70555 respectively.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                             Newcastle disease virus haemagglutinin
                                                                                                                          05-MAY-1997
                                                                                                                                                      AAW10690;
                                                                                                                                                                                AAW10690 standard; Protein;
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Similarity 96.9%;
58; Conservative
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Pred. No. 7e-275;
8; Mismatches 10;
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Fowlpox virus; immunisation; !

; FPV; recombinant virus; vector; vac NDV; haemagglutinin; fusion protein;

poultry.

Newcastle disease

virus

WO9640880-A1

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine antigens to poultry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 107-108; 134pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant fowlpox virus - contg. a foreign DNA inserted into the fowlpox virus genome, used for the
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                                                                                                                             GRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSYF
                                                                                                                                                                       VGGGSFIDGRVWFSVYGGLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYKP
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            CLSIAEISNTLFGEFRIVPLLVEILKNDGVREARSG
                                            HTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKTY
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                                                                                                                                                                                                                 ATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYPG
                                                                                                                                                                                                                                                         ATHYCYTHNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSVS
                                                                                                                                                                                                                                                                                    GWGAPIHDPDYIGGIGKELIVDDASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDMS
                                                                                                                                                                                                                                                                                                          GWGAPIHDPDFIGGIGKELIVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDMS
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                                HTLRGVFGTMLDGEQARLNPASAVFDSTSRSRITRVSSSSIKAAYTTSTCFKVVKTNKTY
                                                                         SPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYRN
                                                                                                                  GRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSYF
                                                                                                                                                           VGGGSFIDSRVWFSVYGGLKPNTPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYKP
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96.9%;
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Pred. No. 7e-275;
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Best Local Similarity
Matches 558; Conserv
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26-FEB-1993;
28-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a recombinant fowlpox virus (FPV) comprising a foreign DNA inserted into a region of the fowlpox virus genome corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a host cell. The virus is used as a vaccine for immunising chickens against Newcastle disease virus (NDV), Fowlpox, and Infectious Laryngotracheitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fowlpox viruses, useful as vaccines for immunization of chickens/turkeys against Fowlpox and Newcastle disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
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Newcastle disease virus; NDV; Fowlpox; Infectious Laryngotracheitis.
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                                                                      RISRAEEKITSALGSNQDVVDRIYKQVALESPLALLNTETTIMNAITSLSYQINGAANNS
                   ATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYPG
                                                                                                                                                   GWGAPIHDPDYIGGIGKELIVDDASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDMS
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                                                                                                                                                                                                                                                                                                                                                                                Conservative
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93US-0024156.
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96.9%;
                                                                                                                                                                                                                                                                                                                                                                            Score 2915; DB 20;
Pred. No. 7e-275;
8; Mismatches 10;
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Query Match
Best Local Similarity
Matches 558; Conserv
                                                                                                                                                                               The present sequence is provided in a specification relating to a recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNA can be expressed in host cells infected with FPV. The recombinant FPV may be used in vaccines to protect animals (especially chickens) against fowlpox and, depending on the source of the foreign DNA, other diseases, particularly Newcastle's disease, Marek's disease or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant fowlpox virus useful as vaccines contains inserted into specific non-essential region of the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6136318-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fowlpox virus; FPV; antiviral; antibacterial; vaccine; Newcastle's disease virus; NDV; Marek's disease;
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                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Column 69-72; 56pp; English.
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28-FEB-1994;
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                                                                                                                                                              laryngotracheitis.
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B; Mismatches 10;
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28-FEB-1994;
                                                                                                      07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                            disease virus.
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                         93US-0024156
94WO-US02252
                                                                                                      95US-0477459
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                                                                                                                                                                                                                                                                                                             VGGGSFIDGRVWFSVYGGLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYPG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATHYCYTHNVILSGCRDHSHSHQYLALGVLRTSATGRVFFSTLRSINLDDTQNRKSCSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 581 AA;
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Pred. No. 7e-275;
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                                                                                                                                                               Query Match
Best Local Sim
Matches 543;
                                                                                                                                                                                                                                   cDNA coding for NDV-derived HN prepared using D-26 strain includes two kinds, one of which is composed of 1746 bp from 112th to 1857th and another is composed of 1848 bp from 112th to 1959th.

(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                              Recombinant avipox virus used as vaccine for fowl having inserted cDNA for Newcastle disease derived haemagglutinin neuraminidase
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAN91000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuraminidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of Newcastle disease virus (NDV) - derived haemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP96147;
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                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                         Disclosure; Fig 4a-4e;
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1989-087599/12.
                                                                                                                                                                                                                                                                                                                                                                                                                Yanagida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-1988;
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21-JAN-1991
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181
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SATHYCYTHNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSV 240
                                    SGWGAPIHDPDFIGGIGKELIVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDM 180
                                                                               TRISRAEEKITSALGSNQDVVDRIYKQVALESPLALLNTETTIMNAITSLSYQINGAANN 120
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                       SGCGAPIHDPDYIGGIGKELIVDDASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDM
                                                                      TAISRTEEKITSALGSNQDVVDRIYKQVALESPLALLNTESTIMNAIKSLSYQINGAANS
                                                                                                                   MDRAVSQVALENDEREAKNTWRLVFRIAILLLTVVTLAISAAALAYSMEASTPSDLVGIP
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                                                                                                                                                                                                               616 AA;
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Saekj S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (updated)
(first entry)
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88JP-0231898
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                                                                                                                                                                            95.0%;
94.1%;
                                                                                                                                                                                                                                                                                                         27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  Ogawa
                                                                                                                                                                  14;
                                                                                                                                                               Score 2847; DB 10;
Pred. No. 3.3e-268;
4; Mismatches 20;
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ID AARO6
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XX DARO6
XX DY 18-DE
XX Powl
XX Haema
XX Newca
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Query Match
                                                         Promoter fragment may be attached to a viral antigen, such as a Newcastle disease antigen eg Haemagglutinin neuraminidase. This may be expressed in a transformed host, to give a stabilised vaccine on a large scale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR06329 standard; protein; 616
                     Sequence
                                                                                                                  Disclosure; Page ?; ?pp; Japanese
                                                                                                                                                                                                                                                                  28-MAR-1989;
29-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                  Fowl pox virus; Newcastles disease antigen; vaccine; haemagglutinin neuraminidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Newcastle disease virus haemagglutinin neuraminidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR06329
                                                                                                                                           Promoter DNA derived from avipox virus, and chimera gene used to produce recombinant avipox virus for vaccine manu
                                                                                                                                                                               WPI; 1990-239051/31.
N-PSDB; AAQ05549.
                                                                                                                                                                                                                  Ogawa R,
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                                              also
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                                              AAQ05544-8.
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                                                                                                                                                                                                                  Yanagida N,
                      616 AA;
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88JP-0335605.
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94.7%;
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Score 2839;
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BB
11;
Length 616;
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                                                                                NHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKT
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                YCLSIAEISNTLFGEFRIVPLLVEILKNDGVREARSG 577
                                                                                                                                                                                                                                                         GVGGGSFIDNRVWFPVYGGLKPNSPSDTAQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYK
                                                                                                                                                                                                                                                                                                                                                                                       SATHYCYTHNVILSGCRDHSHSHQYLALGVLRTSATGRVFFSTLRSINVDDTQNRKSCSV
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                                                               NDTLRGVFGTMLDDEQARLNPVSAVFDSISRSRITRVSSSSTKAAYTTSTCFKVVKTNKT 540
                                                                                                                            FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSVACQASARCPNSCVTGVYTDPYPLVFYR
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                                                                                                                                              FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR 480
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YCLSIAEISNTLFGEFRIVPLLVEILKDDGVREARSG
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16; Mismatches 20;
577
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Search completed: January 2, 2004, 16:18:24 Job time: 59 secs

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Database :
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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                                                                                                                                                                                                                                                                                      283308 segs, 96168682 residues
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2998
1 MDRAVSQVALENDEREAKNT.....IVPLLVEILKNDGVREARSG 577
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19					14	13	12	11	10	9	8	7	6	ហ	.4	u	2	н	Result	
765	766	770	771	772	777	778	781	838	842	2666	2711	2719.5	2738.5	2746	2751	2758	2759	2763	2846	2848	2849	2862	2871	2913	2914	2920	2945	2989	Score	
25.5	25.6	25.7	25.7	•	•	26.0	26.1	•	28.1	•	90.4		91.3		91.8		92.0	92.2	•	95.0	95.0	•	•	97.2		•	98.2	99.7	Query Match I	
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hemagglutinin-neur	HN protein - Muray	hemagglutinin-neur	ption																											

ALIGNMENTS

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RESULT 2
G46328
hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease vi
C;Species: Newcastle disease virus
C;Species: Newcastle disease virus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
C;Accession: G46328; A29201
R;Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Inocencio, N.M.; Kuma,
Virology 169, 260-272, 1989
A;Title: Newcastle disease virus evolution. I. Multiple lineage
A;Reference number: A46328; MUID:89204897; PMID:2705297
A;Accession: G46328
A;Molecule type: mRNA
A;Residues: 1-577 <SAK'>
A;Cross-references: GB:M24711
A;Experimental source: strain TEX/48
R;Schaper, U.M.; Fuller, F.J.; Ward, M.D.W.; Mehrotra, Y.; Stor
Virology 165, 291-295, 1988
A;Title: Nucleotide sequence of the envelope protein genes of a;Accession: A29201
A;Molecule type: mRNA
A;Residues: 1-577 <SCH'>
A;Accession: A29201
A;Molecule type: mRNA
A;Residues: 1-577 <SCH'>
A;Experimental source: strain Texas G.B.
C;Genetics:
A;Gene: HN
C;Superfamily: paramyxovirus hemagglutinin-neuraminidase
C;Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase
F;27-48/Domain: transmembrane #status predicted <TMN'>
F;119,341,433,481,538/Binding site: carbohydrate (Asm) (covaler
                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 566
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Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; t;27-48/Domain: transmembrane #status predicted <TMN>;119,341,433,481,538/Binding site: carbohydrate (Asn) (covalent)
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98.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-577 <SAK>
A;Cross-references: GB:M24708
C;Genetics:
A;Gene: HN
C;Superfamily: paramyxovirus hemagglutinin-neuraminidase
C;Superfamily: paramyxovirus hemagglutinin; hydrolase; t
C;Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; t
F;27-48/Domain: transmembrane #status predicted <TMN>
F;21-48/Johain: transmembrane #status predicted <TMN>
C;Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; t
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Local Similarity 96.9%;
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Pred. No. 8.7e-217;
8; Mismatches 10;
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A;Molecule type: mRNA
A;Residues: 1-577 <JOR>
A;Cross-references: GB:M16573; NID:g332355;
C;Genetics:
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R;Jorgensen, E.D.; Collins, P.L.; Lomedico, P.T.
Virology 156, 12-24, 1987
A;Title: Cloning and nucleotide sequence of Newcastle disease
A;Reference number: A26355; MUID:87122141; PMID:3027962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hemagglutinin-neuraminidase (EC 3.2.1.-) (version 2 C;Species: Newcastle disease virus C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 C:Drossion, 37-35
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;Reywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane
;27-50/Domain: transmembrane #status predicted <TMN>
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A;Cross-references: GB:C;Genetics:
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RESULT 5

R46328

hemagglutinin-neuraminidase (BC 3.2.1.-) - Newcastle disease virus (strain LAS/46)

C.Species: Newcastle disease virus

C.Species: Newcastle disease virus

C.Accession: E46328

R;Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Inocencio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y.

Virology 169, 260-272, 1989

A;Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence vari
A;Reference number: A46328; MUID:89204897; PMID:2705297

A;Accession: E46328
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C;Superfamily: paramyxovirus hemagglutinin-neuraminidase
C;Superfamily: paramyxovirus hemagglutinin-neuraminidase
C;Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane
F;27-48/Domain: transmembrane #status predicted <TMN>
F;119,341,433,481,538/Binding site: carbohydrate (Asn) (covalent) #status predi
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RESULT 6
A46328
hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus (strain D26.7
C;Species: Newcastle disease virus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C;Accession: A46328
R;Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Inocencio, N.M.; Kuma, K.; Miyata, T.; N
Virology 169, 260-272, 1989
A;Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequ
A;Reference number: A46328; MUID:89204897; pMID:2705297
A;Accession: A46328
A;Molecule type: mRNA
A;Residues: 1-616 <SAK>
A;Cross-references: GB:M24705; NID:g332329; PIDN:AAA46655.1; PID:g332330
C;Genetics:
A;Gene: HN
C;Superfamily: paramyxovirus hemagglutinin-neuraminidase
C;Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane price files for the first transmembrane fo
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Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane;27-48/Domain: transmembrane #status predicted <TMN>;119,341,433,481,538,600/Binding site: carbohydrate (Asn) (covalent) #status p
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Pred. No. 5.7e-213;
5; Mismatches 16;
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R;Sakaguchi,
Virology 169,
A;Title: Newc
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C46328
                hemagglutinin-neuraminidase (EC 3.2.1.-) - C;Species: Newcastle disease virus C;Date: 31-Dec-1993 #sequence_revision 31-E C;Accession: C46328 R;Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Inc Virology 169, 260-272, 1989
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A;Reference number: A92799; MUID:88171450; PMID:3351479
A;Accession: B29823
A;Molecule type: mENA
A;Residues: 1-616 <MIL>
A;Cross-references: GB:D00243; NID:g222174; PIDN:BAA00174.1; PID:C;Genetics:
C;Genetics:
C;Genetics:
A;Gene: HN
C;Superfamily: paramyxovirus hemagglutinin-neuraminidase
C;Superfamily: paramyxovirus hemagglutinin; hydrolase;
F;27-54/Domain: transmembrane #status predicted <TMN>
F;119,341,433,481,538,600/Binding site: carbohydrate (Asn) (coval
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C;Date: 30-Jun-1989 #sequence_revision:
C;Accession: B29823
R;Millar, N.S.; Chambers, P.; Emmerson,
J. Gen. Virol. 69, 613-620, 1988
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Best Local Similarity
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;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989
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                   YCLSIAEISNTLFGEFRIVPLLVEILKNDGVREARSG
                                                                  NHTLRGVFGTMLDDKQARLNPVSAVFDSISRSRITRVSSSSTKAAYTTSTCFKVVKTNKT
                                                                                        NHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKT
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Pred. No. 2.8e-212;
8; Mismatches 15;
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31-Dec-1993

#text_change 15-Oct-1996

Newcastle

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Inocencio, N.M.;

Kuma,

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Miyata, T.;

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C;Date: 31-Dec-1993 #sequence_revision 31-De
C;Accession: B46328
R;Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Inox
Virology 169, 260-272, 1989
A;Title: Newcastle disease virus evolution.
A;Reference number: A46328; MUID:89204897; I
A;Accession: B46328
                                                                                                                                             hemagglutinin-neuraminidase (EC 3.2.1.-)
C;Species: Newcastle disease virus
C;Date: 31-Dec-1993 #sequence_revision 31
C;Accession: B46328
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A; Residues: 1-616 <SAK>
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;Cross-references: GB:M24706;
;Genetics:
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Accession: C46328
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                        NID:g332331; PIDN:AAA46656.1;
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Pred. No. 2.8e-211;
8; Mismatches 17;
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                                                                                                                              Inocencio,
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                                                                                  . I. Multiple lineages
PMID:2705297
                                                                                                                                                                                         Newcastle
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                        PID:g332332
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C;Superfamily: paramyxovirus hemagglutinin-neuraminidase
C;Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane
F;27-48/Domain: transmembrane #status predicted <TMN>
F;119,341,433,481,538,600/Binding site: carbohydrate (Asn) (covalent) #status predicted (Asn)
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                                                                                                                      FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR
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94.1%;
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Pred. No. 3
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A;Gene: HN
C;Superfami
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HNNZQD
HNNZQD
C;Species: Newcastle disease virus
C;Species: Newcastle disease virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 1
C;Accession: A31110
R;Gorman, J.J.; Nestorowicz, A.; Mitchell, S.J.; Corino, G.L.; Se J. Biol. Chem. 263, 12522-12531, 1988
A;Title: Characterization of the sites of proteolytic activation
A;Reference number: A92665; MUID:88315049; PMID:3045120
                                                                                                                                                                                  A;Accession: A31110
A;Molecule type: genomic
A;Residues: 1-616 <GOR>
C;Superfamily: paramyxovirus hemagglutinin-neuraminidase
C;Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane
F;1-574/product: hemagglutinin-neuraminidase #status predicted <HNS>
F;27-54/Domain: transmembrane #status predicted <TMN>
                                                                                                                                                          A;Residues: 1-616 <GOR>
A;Cross-references: GB:J03911;
                                                                                                                                      ;Genetics:
                                                                                                                                                          NID:g332327; PIDN:AAA46654.1;
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F;119,341,433,481,538,600/Binding

site:

carbohydrate

(Asn)

(covalent)

#status

predicted

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RESULT 11

A36829

hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus (str C;Species: Newcastle disease virus

C;Species: Newcastle disease virus

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Oct-C;Accession: A36829

R;Sakaguchi, T; Toyoda, T; Gotoh, B; Inocencio, N.M.; Kuma, K.; Miya Virology 169, 260-272, 1989

A;Title: Newcastle disease virus evolution. I. Multiple lineages define A;Reference number: A46328; MUID:89204897; PMID:2705297

A;Accession: A36829

A;Molecule type: mRNA
A;Residues: 1-571 <SAK>
A;Cross-references: GB:M24714

C;Genetics:
                                                                                                                 C;Genetics:
A;Gene: HN
A;Gene: HN
C;Superfamily: paramyxovirus hemagglutinin-neuraminidase
C;Keywords: glycoprotein; glycosidase; hemagglutinin; hyc
F;27-48/Domain: transmembrane #status predicted <TMN>
F;119,341,433,481,508,538/Binding site: carbohydrate (Ass
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Best Local S
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ilarity 91.6%;
Conservative 2.
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; Pred. No. 1.1e
24; Mismatches
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9; Mismatches 16;
                                                                   ; DB 1;
1.1e-204;
nes 24;
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C;Species: Newcastle disease virus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_cha
C;Accession: 146328
R;Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Inocencio, N.M.; Kum
Virology 169, 260-272, 1989
A;Title: Newcastle disease virus evolution. I. Multiple line
A;Reference number: A46328; MUID:89204897; PMID:2705297
A;Accession: 146328
A;Molecule type: mRNA
A;Residues: 1-571 <SAK>
A;Cross-references: GB:M24713
C;Genetics:
A;Genetics
C;Superfamily: paramyxovirus hemagglutinin-neuraminidase
C;Reywords: glycoprotein; glycosidase; hemagglutinin; hydrol
F;27-48/Domain: transmembrane #status predicted <TMN>
F;119,341,433,481,508,538/Binding site: carbohydrate (Asn)
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                                                                                                                                                                  Conservative
                                                                                                                                                                               92.0%;
                                                                                                                                                                   Score 2759; DB 1;
Pred. No. 2.1e-204;
2; Mismatches 26;
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A; Molecule type: mRNA
A; Residues: 1-2, 'LP', 5-52, 'S', 54-215, 'A', 217-399, 'AD', 402-571 <SAK>
A; Cross-references: GB:M24715
A; Experimental source: strain ITA/45
C; Genetics:
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C;Superf
C;Keywor
F;27-48/
F;119,34
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R;Wemers, C.D.; de Henau, S.; Neyt, C.; Espion, D.; Letellier, C.; Meulemans, Arch. Virol. 97, 101-113, 1987
A;Title: The hemagglutinin-neuraminidase (HN) gene of Newcastle disease virus A;Reference number: S07126; MUID:88076411; PMID:3318761
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A;Molecule type: mRNA
A;Residues: 1-571 <WEM>
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Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein;27-48/Domain: transmembrane #status predicted <TMM>;19,341,433,481,508,538/Binding site: carbohydrate (Asn) (covalent) #status predicted;
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                                                                                                                                                       Conservative
                                                                                                                                                                     92.0%;
91.1%;
                                                                                                                                                                   Score 2758; DB 1;
Pred. No. 2.6e-204;
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PMID:3318761
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C;Accession: H46328
R;Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Inocencio, N.M.;
Virology 169, 260-272, 1989
A;Title: Newcastle disease virus evolution. I. Multiple
A;Reference number: A46328; MUID:89204897; PMID:2705297 A; Molecule type: mRNA A; Residues: 1-571 < SAK> hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus (strain AUS/32) C;Species: Newcastle disease virus (C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Oct-1996 A; Accession: H46328 N.M.; Kuma, lineages defined by K.; Miyata, T.; Nagai, sequence vari

A;Cross-references: GB:M24712 C;Genetics: Ħ

C;Superfamily: paramyxovirus hemagglutinin-neuraminidase C;Keywords: glycoprocein; glycosidase; hemagglutinin; hydrolase; transmembrane F;27-48/Domain: transmembrane #status predicted <TWN> F;119,341,433,481,508,538/Binding site: carbohydrate (Asn) (covalent) #status p Score 2751; DB 1; Length predicted

Matches Query Match Best Local 181 121 121 522; 61 13 Similarity MDRAVSQVALENDEREAKNTWRLIFRIAILLLIVVTLATSVASLVYSMGASTPSDLVGIP SATHYCYTHNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSV SGWGAPIHDPDFIGGIGKELIVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDM TRISRABEKITSALGSNQDVVDRIYKQVALESPLALLNTETTIMNAITSLSYQINGAANN 120 SGCGAPVHDPDYIGGIGKELIVDDTSDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDM TAISRAEGKITSALGSNQDVVDRIYKQVALESPLALLNTESIIMNAITSLSYQINGAANN Conservative 91.8%; 91.4%; ; Pred. No. 8.8e 23; Mismatches No. 8.8e-204; Indels 0 Gaps 180 60 240 180 60 0

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gene of newca	hemagglutinin-neuraminidase - Newcastle disease virus C;Species: Newcastle disease virus C;Dete: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999 C;Accession: S40164 R;Kallman, A.; Zadori, Z.; Kisari, J.; Fodor, I. submitted to the EMBL Data Library, May 1993 A;Description: Nucleotide sequence of the hemagglutinin-neuraminidase (HN) A;Reference number: S40163 A;Accession: S40164 A;Status: preliminary A;Molecule type: genomic RNA A;Residues: 1-571 <kal-s a;cross-references:="" c;superfamily:="" embl:x71994;="" hemagglutinin-neuraminidase<="" nid:g437888;="" paramyxovirus="" pid:g437889="" pidn:caa50868.1;="" td=""><td>hema C;Sp C;Apa C;Apa R;Ka B;De A;Re A;St A;St A;St C;Su</td></kal-s>	hema C;Sp C;Apa C;Apa R;Ka B;De A;Re A;St A;St A;St C;Su
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SWISS-PROT entry is copyright. It sen the Swiss Institute of Bioinfo Muropean Bioinformatics Institute, by non-profit institutions as lower its and this statement is not removine and this statement agreement (incompanies requires a license@isb-sib.ch)	"TION: HEMAGGLUTININ IS RESPONSIBLE TIELL RECEPTORS AND FOR INITIATING IN VITY HELPS THE EFFICIENT SPREAD OF MATURE VIRIONS FROM THE NEURAMINIC COPROTEINS. ALYTIC ACTIVITY: Hydrolysis of alphia-(2-8)-glycosidic linkages of te: gosaccharides, glycoproteins, glyco- hetic substrates EELJULAR LOCATION: EXTERNAL, ANCHORI ERMINAL HYDROPHOBIC SEQUENCE. LLARITY: BELONGS TO THE PARAMYXOVIR ZAMNINDASE FAMILY.	529 oh lut			ed) sequence annotatio	PRT;	HEMA PI3HW HEMA PI3HW HEMA PI3HV HEMA PI3HA HEMA PI1HA HEMA PI1HA PM20 CHLPN PRY3 YEAST MU5B HUMAN YN96 YEAST CDH PHACH HEMA MUMPS YFGG_SCHPO
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AC P12553;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
GN HN.
OS Newcastle disease virus (strain Texas g.b./48) (CViruses; sSRNA negative-strand viruses; Mononegator Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OK NCBI_TaxID=11189;
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CYTOPLASMIC (POTENTIAL).

POTENTIAL.

EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. . .) (POON-LINKED (GLCNAC. . .) (PO
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Pred. No. 8.5e
1; Mismatches
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1D4C52B4887ECIA1 CRC64;
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Similarity

98.0%; 97.9%;

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565;

Conservative

5

Score 2938; D Pred. No. 9.2e 5; Mismatches

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SATHYCYTHNIISSGCRDHSHSYQYLALGVLRTSATGRIFFSTLRSINLDDTQNRKSCSV SATHYCYTHNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSV SGWGAPIHDPDFIGGIGKELIVDDASDVTSFYPSAFQEHHNFIPAPTTGSGCIRIPSFDM SGWGAPIHDPDFIGGIGKELIVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDM TRISRAEEKITSALGSNQDVVDRIYKQVALESPLALLNTETTIMNAITSLSYQINGAANN TRISRAEEKITSALGSNQDVVDRIYKQVALESPLALLNTETTIMNAITSLSYQINGAANN

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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence variability of the Virology 169:260-272 (1989).
-!- FUNCTION: HEMAGGLUTININ TO CELL RECEPTORS AND FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=88265873; PubMed=3388773; Schaper U.M., Fuller F.J., Ward M.D.W., Mehrotra 'Stripp B.R., de Buysscher E.V.; Wircleotide sequence of the envelope protein genes virulent, neurotropic strain of Newcastle disease Virology 165:291-295(1988).
                                                                                                                                                                                                                                  EMBL; M21409; AAA4669.1; -.
EMBL; M24711; AAA46661.1; -.
InterPro; IPR000665; Hem-neuramndse.
Pfam; PF00423; HN; 1.
                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=89204897; PubMed=2705297;
MCDLINE=89204897; PubMed=2705297;
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                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                 Hydrolase; Hemagglutinin;
                                                                                                                                                                                                 Fransmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING THE MATTER VIRIONS FROM THE NEURAMINIC ACID CONTAINING GLYCOPROTEINS.

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.

SUBJECTIVILAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS N-TERMINAL HYDROPHOBIC SEQUENCE.

SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEURAMINIDASE FAMILY.
26
48
577
119
341
434
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538
481
538
332
63275
                                                                                                                                                                                                                Envelope protein; Glycoprotein;
   POTENTIAL.

EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. . .) (PO')

H -> L (IN REF. 2).

E -> R (IN REF. 2).

E -> R (IN REF. 2).
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                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
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HEMA NOVH4

ID HEMA NOVH4

AC P1255; P06158;

DT 01-0CT-1989 (Rel. 12, Created)

DT 01-0CT-1989 (Rel. 12, Last sequence update)

DT 01-0CT-2001 (Rel. 40, Last annotation update)

DT 16-0CT-2001 (Rel. 40, Last annotation update)

DE Hemagglutinin-neuraminidase (EC 3.2.1.18).

GN NA

OS Newcastle disease virus (strain B1-Hitchner/47)

OC Viruses; serNa negative-strand viruses; Mononegai

OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.

OX NCBI_TaxID=11181;

RN [1]

RP SEQUENCE FROM N.A.

REDLINE=87122141; PubMed=3027962;

RA JOZGENSEN E.D., Collins P.L., Lomedico P.T.;

RA WEDLINE=89104897; PubMed=3027962;

RA WEDLINE=89204897; PubMed=2705297;

RA SARAGUCHI T., TOYODA T., GOTCH B., Inocencio N.M.

RA Nagai Y.;

RY "Newcastle disease virus evolution. I. Multiple

RT "Newcastle disease virus evolution. I. Multiple

CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR A

CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO

NETHEMANINDASE FAMILY.

CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO

NETHEMANINDASE FAMILY.

CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO

NETHEMANINDASE FAMILY.

CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO

NETHEMANINDASE FAMILY.

C
                                                                                                                        RA Sakaguchi T., Toyoda T., Gotoh B., Inocencio N.M., Kuma K., Miyata T., RA Nagai Y.;
RA Nagai Y.;
Recastle disease virus evolution. I. Multiple lineages defined by sequence variability of the hemagglutinin-neuraminidase gene.";
RECEDIORS 169:260-272(1989).
C. INTOLOGY 169:260-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=87122141; PubMed=3027962;

Jorgensen E.D., Collins P.L., Lomedico P.T.;

"Cloning and nucleotide sequence of Newcastle disease virus "Cloning and nucleotide sequence of Newcastle disease virus hemagglutinin-neuraminidase mRNA; identification of a putative acid binding site.";

Virology 156:12-24(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Newcastle disease virus (strain B1-Hitchner/47) (NDV).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI_TaxID=11181;
          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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Pfam; PF00423; HN; 1.
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EMBL; M24708; AAA46658.1;
PIR; A26355; HNNZNC.
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EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC...) (PO
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Pred. No. 7.3e
8; Mismatches
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-> S (IN REF. 2).
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SEQUENCE FROM N.A.
MEDLINE-89204897; PubMed=2705297;
MEDLINE-89204897; PubMed=2705297; PubMed=270529
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-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE ACTIVITY HELDS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING THE MATURE VIRIONS FROM THE BUURAMINIC ACID CONTAINING GLYCOPROTEINS.

-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-, alpha-(2-8)-glycoproteins, glycolipids, colominic acid and synthetic substrates.

-!- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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InterPro; IPR000665; Hem-neuramndse
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SIMILARITY: BELONGS TO THE PARA
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(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
in-neuraminidase (EC 3.2.1.18).
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Pred. No. 8
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P12555,
01-OCT-1989 (Rel. 12, C
01-OCT-1989 (Rel. 12, I
16-OCT-2001 (Rel. 40, I
                                                                                                                                                                     "Newcastle disease virus evolution. I. Multiple lineages defined by sequence variability of the hemagglutinin-neuraminidase gene."; Virology 169:260-272(1989).

-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATIN THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Newcastle disease virus (strain D26/76) (NDV).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI_TaxID=11180;
                                                                                                                                           <del>-</del>
                                                                                                                                                                                                                                                                                                MEDLINE=89204897; PubMed=2705297;
Sakaguchi T., Toyoda T., Gotoh B., Inocencio N.M.,
                                                                                                                                                                                                                                                                                                                                                                           "Structural features unique to each of the three antigenic sites the hemagglutinin neuraminidase protein of Newcastle disease viru
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=88160043; PubMed=2450424;
Gotoh B., Sakaguchi T., Nishikawa K.,
Toyoda T., Nagai Y.;
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16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin-neuraminidase (EC 3.2.1.18).
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                                                                                                     GLYCOPROTEINS.

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->8)-glycosidic linkages oligosaccharides, glycoproteins,
                                             N-TERMINAL HYDROPHOBIC SEQUENCE SIMILARITY: BELONGS TO THE PARA
                                                                           synthetic substrates.
SUBCELLULAR LOCATION: EXTERNAL,
                               NEURAMINIDASE FAMILY.
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DOMAIN
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EMBL; M24705; AAA46655.1; -.
PIR; A46328; A46328.
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Hydrolase;
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PF00423; HN; 1.
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EXTRACELLULAR (POTENTIAL)
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RT sequence variability of the hemagglutinin-neuraminidase gene.";

VIFOLOGY 169:260-272(1989).

C: FUNCTION: HEMAGGLUTININ I RESPONSIBLE FOR ATTACHING THE VIRUS
C: TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
C: ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
C: GLYCOPROTEINS.
C:-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
-!- SUBCELULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
N-TERMINAL HYDROPHOBIC SEQUENCE.
-!- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
NEURAMINIDASE FAMILY
                                                                                                                           EMBL; D00243; BAA00174.1; -.
EMBL; M19478; AAA46677.1; -.
EMBL; M24707; AAA46657.1; -.
EMBL; A03672; CAA00292.1; -.
PIR; B29823; HNNZU.
PIR; C46328; C46328.
InterPro; IPR000665; Hem-neura
Pfam; PF00423; HN; 1.
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P12558;
01-OCT-1989
01-OCT-1989
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-89204897; PubMed=2705297;
Sakaguchi T., Toyoda T., Gotoh B., 1
Nagai Y.;
"Newcastle disease virus evolution."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gotoh B., Sakaguchi T., Nishikav Toyoda T., Nagai Y.;
"Structural features unique to the hemagglutinin-neuraminidase Virology 163:174-182(1988).
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SEQUENCE FROM N.A.
MEDLINE=88160043; PubMed=2450424;
MEDLINE=89160043; Nishikawa
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"Nucleotide sequence of the fusion and haemagglutinin-neuraminidase glycoprotein genes of Newcastle disease virus, strain Ulster: molecular basis for variations in pathogenicity between strains.";
J. Gen. Virol. 69:613-620(1988).
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MEDLINE=88171450; PubMed=3351479;
MILLAR N.S., Chambers P., Emmerso
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                                                                                                Transmembrane.
                                                                                                              Hydrolase; Hemagglutinin;
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(Rel. 12, Last sequence update)
(Rel. 40, Last annotation updat
in-neuraminidase (EC 3.2.1.18)
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CYTOPLASMIC (POTENTIAL).

POTENTIAL.

EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)
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01-JAN-1990 (Rel. 13, Last s
16-OCT-2001 (Rel. 40, Last a
Hemagglutinin-neuraminidase
             SEQUENCE FROM N.A.
MEDLINE=88315049; PubMed=3045120;
Gorman J.J., Nestorowicz A., Mitchell S.J.,
                                                                           Newcastle disease virus (strain Queensland/66) (NDV).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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in-neuraminidase (EC 3.2.1.18).
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L -> S (IN REF. 2)
L -> H (IN REF. 2)
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L -> R (IN REF. 2)
L -> R (IN REF. 2)
K -> E (IN REF. 2)
K -> G (IN REF. 2)
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Envelope protein; Glycoprotein

CYTOPLASMIC (POTENTIAL).
POTENTIAL.

EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-S Q (IN REF. 2).

Y-S F (IN REF. 2).

X-S G (IN REF. 2).

X-S G (IN REF. 2).

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CRC64;

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EMBL; J03911; AAA46654.1; -.
EMBL; M24706; AAA46656.1; -.
PIR; A31110; HNNZQD.
PIR; B46328; B46328.
InterPro; IPR000665; Hem-neuramndse.
Pfam; PF00423; HN; 1.
Hydrolase; Hemagglutinin; Envelope pro
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"Newcastle disease virus evolution. I. multiple lineages
"Newcastle disease" of the hemagination of the hemagi
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MEDLINE=89204897; PubMed=2705297;
Sakaguchi T., Toyoda T., Gotoh B.,
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CAPALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal stalic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.

SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS N-TERMINAL HYDROPHOBIC SEQUENCE.

SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
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                                                                                                                                        Conservative
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                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=89204897; Sakaguchi T., Toyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin-neuraminidase (EC 3.2.1.18).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Newcastle disease virus (strain Her/33) (NDV).
                                                                                                                                                       FUNCTION: HEMAGGIUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING GLYCOPROTEINS.

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-dycosidic linkages of terminal stablic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.

SUMCIAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS N-TERMINAL HYDROPHOBIC SEQUENCE.

SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
                                                                                                                                                NEURAMINIDASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                         Gotoh B.,
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HEMA NDVM STANDARD; PRT; 571 AA. P12557; O1-OCT-1989 (Rel. 12, Created) O1-OCT-1989 (Rel. 12, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hemagglutinin-neuraminidase (EC 3.2.1.18).

Newcastle disease virus (strain Miyadera/51) (NDV). Viruses; ssRNA negative-strand viruses; Mononegavirales;

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Pfam; PF00423; HN; 1
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                                                      NHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKT
                                                                                           FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR
                                                                                                                                      PGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY
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POTENTIAL.
EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Newcastle disease virus evolution. I. Multiple lineages defined by sequence variability of the hemagglutinin-neuraminidase gene."; Virology 169:260-272(1989).

-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION. MEURAMINDASE ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING GLYCOPROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sakaguchi T., Toyoda
Nagai Y.;
                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                      CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000665; Hem-neuramndse
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ology 163:174-182(1988).
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SIMILARITY: BELONGS TO THE PARAI
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SUBCELLULAR LOCATION:
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            SGWGAPIHDPDFIGGIGKELIVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDM
                                                                 TRISRAEEKITSALGSNQDVVDRIYKQVALESPLALLNTETTIMNAITSLSYQINGAANN
SGCGAPVHDPDYIGGIGKELIVDDASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDM
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EXTRACELLULAR (POTENTIAL).

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N-LINKED (GLCNAC...) (POT
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Pred. No. 1.1e-210
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tein of Newcastle disease
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                   Length 571;
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SEQUENCE FROM N.A.
MEDLINE=89204897; PubMed=2705297;
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01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                       strain Italien (NDV Italien): comparison with and expression by a vaccinia recombinant."; Arch. Virol. 97:101-113(1987).
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MEDLINE-88076411; PubMed=3318761;
Wemers C.D., de Henau S., Neyt C.,
Meulemans G., Burny A.;
                                                                                                                                                                                                                                                                                                                                    Newcastle disease virus (strain Italien/45) (NDV)
Viruses; ssRNA negative-strand viruses; Mononegav
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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Pfam; PF00423; HN; 1.
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or send an email to license@isb-sib.ch).
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N-LINKED (GLCNAC. .) (POTENTIAL).
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F1ECB12BEF46C00F CRC64;
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01-OCT-1989
01-JUN-1994
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P12554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Newcastle disease virus evolution. I. Multiple lineages defined by sequence variability of the hemagglutinin-neuraminidase gene."; Virology 169:260-272(1989).

-i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McGinnes L.W., Wilde A., Morrison T.G.;
"Nucleotide sequence of the gene encoding the Newcastle hemagglutinin-neuraminidase protein and comparisons of phemagglutinin-neuraminidase protein sequences.";
Virus Res. 7:187-202(1987).
   Transmembrane.
1 TRANSMEM 27
TRANSMEM 27
DOMAIN 49
CARBOHYD 119
CARBOHYD 340
                                                                                                                                    EMBL; M22110; AAA46670.1;
EMBL; M24712; AAA46662.1;
PIR; B31110; HNNZAV.
                                                                                                                                                                                                entities requires a license agreement (Some send an email to license@isb-sib.ch).
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Nagai Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Newcastle disease virus (strain Australia-Victoria/32) (NDV).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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                                                                                                                                                                                                                                modified
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MEDLINE=89204897; PubMed=2705297;
Tovoda T., Gotoh B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=88315049;
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                                                                DOMAIN
                                                                                                           Pfam;
                                                                                                                         InterPro;
                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EWBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                      N-TERMINAL HYDROPHOBIC SEQUENCE. SIMILARITY: BELONGS TO THE PARAN NEURAMINIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                  synthetic substrates.
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                               GLYCOPROTEINS.

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and
                                                                                                           PF00423; HN;
                                                                                                                         IPR000665; Hem-neuramndse
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                                                                                         Envelope protein; Glycoprotein;
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annotation update)
e (EC 3.2.1.18).
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Matches 521
                                                          Newcastle disease virus (strain Chi/85) (NDV)
Viruses; ssRNA negative-strand viruses; Monone
Paramyxoviridae; Paramyxovirinae; Rubulavirus
NCBI_TaxID=11179;
                                                                                                     LT 12

HEMA NDVC STANDARD; PRT; 571 AA. P35740;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin-neuraminidase (EC 3.2.1.18).
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SEQUENCE
                    SEQUENCE FROM N.A.

MEDLINE=89204897; PubMed=2705297;

Sakaguchi T., Toyoda T., Gotoh B.,

Nagai Y.;
            Newcastle disease
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21; Conservative
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H-> HY (IN REF. 1).

D-> H (IN REF. 1).

E-> Q (IN REF. 1).
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           Multiple lineages
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                                                                                                                               STTHYCYTHNVILSGCRDHSHSHQYLALGVLRTSATGRVFFSTLRSINLDDTQNRKSCSV
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            FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR
                                                                                               SATPLGCDMLCSKVTETEEEDYKSVTPTSMVHGRLGFDGQYHEKDLDTTVLFKDWVANYP
                                                                                                                                                                  SGCGEPVHDPDYIGGIGKELIVDDISDVTSFYPSAYQEHLNFIPAPTTGSGCTRIPSFDM
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240

240 180 180 120

480

420 360 360

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120

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Sequence variability of the hemagglutinin-neuraminidase gene.";

L Virology 169:260-272(1989).

C -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
C THE MATURE VIRIONS HOW THE NEURAMINIC ACID CONTAINING
C GLYCOPROTEINS.

C -!- CATALYTIC ACTIVITY. Hydrolysis of alpha-(2->3)., alpha-(2->6).,
alpha-(2->8).glycopidic linkages of terminal sialic residues in
c alpha-(2->8).glycoproteins, glycolipids, colominic acid and
c synthetic substrates.

C -!- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
C -!- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
NEURAMINIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      PIR; C36829; C36829.
InterPro; IPR000665; Hem-neuramndse.
Pfam; PF00423; HN; 1
                                                                                                                                                                                                                                                                                                                                  Hydrolase; Hemagglutinin;
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M24716; AAA46666.1;
                                                                                                                                                                                                                                                                                                            Transmembrane.
al Similarity
507; Conserv
                                                                                                                                        1
27
49
119
341
433
481
    Conservative
                                                        26
27
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49
571
1341
433
481
508
62901 WW;
                        90.4%;
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  32;
                                                                                        CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
Score 2711; D
Pred. No. 8.4e
32; Mismatches
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                          .4e-207
                                                DB
                                              Length
    Indels
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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16-OCT-2001
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SEQUENCE FROM N.A.
MEDLINE=89204897; PubMed=2705297;
MEDLINE=89204897; PubMed=2705297;
MEDLINE=89204897; PubMed=2705297;
MEDLINE=89204897; PubMed=2705297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Newcastle disease virus evolution. I. Multiple lineages defined by sequence variability of the hemagglutinin-neuraminidase gene."; Virology 169:260-272(1989).

-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE ACTIVITY HELDS THE BEFICIENT SPREAD OF THE VIRUS BY DISSOCIATING THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000665; Hem-neuramndse.
Pfam; PF00423; HN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M24717; AAA46667.1; PIR; D36829; D36829.
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Nagai Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Newcastle disease virus (strain Iba/85) (NDV).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES
NEURAMINIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYCOPROTEINS.

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal stalic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetic substrates.
SUBCELLULAR LOCATION: EXTERNAL,
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(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
                Conservative
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             34;
                                                                                                                                   POTENTIAL.

EXTRACELULAR (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
           Score 2666; D
Pred. No. 3.1e
34; Mismatches
                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
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(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
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           <u>,</u>
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VITOLOGY 179:738-748(1990).

-i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS FOR CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING GIXCOPROTEINS.

-i- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEMA SV41
P25180;
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Toshiba/Chanock;
MEDLINE=91049440; PubMed=2173260;
Tsurudome M., Bando H., Nishio M.,
                                                                                                                                                                                                                                                     virus.";
                                                                                                                                                                                                                                                                                                  Komada H., Ito Y.;
"Antigenic and structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Rubulavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simian virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hemagglutinin-neuraminidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1992
16-OCT-2001
                                                                                                                                                                                                                                                                            ntigenic and structural properties of a particular (SV41) reveal a close relationship with
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(Rel. 22,
(Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ptam;
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SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO N-TERMINAL HYDROPHOBIC SEQUENCE.
SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEURAMINIDASE FAMILY.
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TTSTCFKVVKTNKTYCLSIAEISNTLFGEFRIVPLLVEIL
                                  MNNPFPAGSSGVNPNYLFGGAF---LWADVARVNPTFYMASATQYKNTTGFPNSNQKAAY
                                                                                                              YKINTDFSQGLPPLIEAQWVPTYLVP-----
                                                                                                                                                                                    RLIQSAVLVCPLSDQLTDQCRVVLFNNSETMMGAEGRLYTIGGDLYYYQRSSSWWTASLL
                                                                                                                                                                                                                                                              YHLGYLAFPVYGGLIQNSAAWNSQFGSYFLPQNPAVQCSGSAEQQINTAKGSYVVNWFSG
                                                                                                                                                                                                                                                                                                                                       YVATKTEQEDYAATTPSEL---RLTF--YYYNETLVERTLTIPNVTGNWATLNPAVGSGV
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                                                                     - FYRNHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAY
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Pred. No. 1.
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N-LINKED (GLCNAC. . .) (F
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Takeuchi K., Tanabayashi K., Hishiyama M., Yamada A., Sugiura A.;
Takeuchi K., Tanabayashi K., Hishiyama M., Yamada A., Sugiura A.;
TCloning and sequencing of the haemagglutinin-neuraminidase gene of mumps virus (Miyahara strain).";
Nucleic Acids Res. 17:5840-5840(1989).
-1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin-neuraminidase (EC 3.2.1.18).
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Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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Pfam; PF00423; HN; 1.
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                                                                                                                                                                                                                                                     Transmembrane.
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CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-
alpha-(2->8)-glycosidic linkages of terminal stalic residues
oligosaccharides, glycoproteins, glycolipids, colominic acid
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SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic substrates.
SUBCELLULAR LOCATION: EXTERNAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEURAMINIDASE FAMILY.
                                                                                                                                                                                                                                                                                                               A34054; HNNZMM.
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Search completed: January 2, 2004, 16:18:50 Job time : 21 secs

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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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SEQUENCE 577 AA;
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Takimoto T., Taylor G.L., Crennell S.J
"Crystallization of Nevcastle disease
"Crystallization of Nevcastle disease
neuraminidase glycoprotein.";
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Gribanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I.,
Gusev A.A., Balyshev V.M., Zhesterev V.I., Vishnjakov I.F.
"Phylogenetic analysis of Newcastle disease virus of Russi
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; Y19020; CAB59911.1; -.
EMBL; Y19726; CAB477272.1; -.
EMBL; Y1926; CAB46667.1; -.
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Gribanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,
Gusev A.A., Balyshev V.M., Zhesterev V.I., Vishnjakov I.F.;
"Phylogenetic analysis of Newcastle disease virus of Russia.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                 SEQUENCE
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI_TaxID=14176;
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                                                                         PF00423;
                                                                                              AJ243386; CAB46067.1; -.
Pro; IPR000665; Hem-neuramndse.
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Query Match
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                                           InterPro; IPROVE
Pfam; PF00423; F
                                                                                           SEQUENCE: STRAIN=BI (SEPRL);
STRAIN=BI (SEPRL);
MEDLINE=96414821; PubMed=8817822;
MEDLINE=96414821; PubMed=8817822;
Seal B.S., King D.J., Bennett J.D.;
Seal B.S., King D.J., Bennett J.D.;
"Characterization of Newcastle disease virus vaccines by biological
"Characterization of Newcastle disease virus vaccines by biological
"Characterization of Newcastle disease virus vaccines by biological
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Q83846;
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                                                                   EMBL; U37193; AAC55047.1; -. InterPro; IPR000665; Hem-neuramndse.
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=11176;
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Score 2920; DI
Pred. No. 4.9e.
8; Mismatches
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Last annotation updat
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9; Mismatches 7;
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            4.9e-231;
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O90340;
01.NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-JUN-2001 (TrEMBLrel. 17,
Hemagglutinin-neuraminidase
                                                                                                                                                                                         STRAIN=LASOTA;

de Leeuw O.S., Peeters B.P.H.;

"Complete nucleotide sequence of Newcastle disease virus: evidence
the existence of a new genus within the subfamily Paramyxovirinae.
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

[2]
                                                                                                                                                                                                                                                                                                                                                            Newcastle disease virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
 SEQUENCE FROM N.A.
Romer-Oberdorfer A.;
Submitted (MAR-1999) to the
EMBL; AF077761; AAC28376.1;
                                                                                                                                   "Generation of reco
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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01-DEC-2001
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                                                    Sellers H.S., Seal B.S.;
"Complete sequence for the B1
Submitted (SEP-2000) to the EN
EMBL; AF309418; AAG36979.1; -.
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Hemagglutinin-neuraminidase.
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                                                                                                                                                                                                         Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Rubulavirus.
InterPro; IPR000665;
Pfam; PF00423; HN; 1.
SEQUENCE 577 AA; 6
 SEQUENCE
                                                                                                                                   STRAIN=B1;
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                                                                                                                                                                                     NCBI_TaxID=11176;
                                                                                                                                                                                                                                            Newcastle disease virus.
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8; Mismatches
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EMBL/GenBank/DDBJ databases.
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Q91AH7; O1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hemagglutinin-neuraminidase.
HN.
                                                                                                                                                           MEDLINE=21548317; PubMed=11689668;
Nakaya T., Cros J., Park M.S., Nakaya
Villar E., Garcia-Sastre A., Palese P.
"Recombinant newcastle disease virus a
J. Virol. 75:11868-11873(2001).
                                                                                                                                                                                                                                                                                                                                 Newcastle disease virus.
Viruses; ssRNA negative-strand viruses; Monono Paramyxoviridae; Paramyxovirinae; Rubulavirus NCBI_TaxID=11176;
                         Nakaya T., Garcia-Sastre A.,
Submitted (MAY-2001) to the
EMBL; AF375823; AAK55551.1;
                                                                                    STRAIN=B1;
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                                                                  "Haemagglutinating activity of the lentogenic strain MET95,"; strain MET95,"; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ EMBL; AY143159; AAN18268.1; - SEQUENCE 577 AA; 63269 MW; 1B3EA9900BB5AF4
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
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STRAIN-vaccine 1;
MEDLINE=96414821; PubMed=8817822;
Seal B.S., King D.J., Bennett J.D.;
"Characterization of Newcastle disease v
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Q83842; Ol-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                   EMBL; U37187; AAC55041.1;
InterPro; IPR000665; Hem-r
Pfam; PF00423; HN; 1.
SEQUENCE 577 AA; 63213
                                                                                                                                                                                                    properties and sequence protein gene.";
Vaccine 14:761-766(1996)
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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                                            STRAIN-SAH/85;
Gribanov O.G., Starov S.K., Lomakin A. Gribanov O.G., Starov V.M., Zhesterev V "Phylogenetic analysis of Newcastle di Submitted (JUN-1999) to the EMBL/GenBaEMBL; Y19021, CABS0912.1; ---
EMBL; AJ243384; CAB46065.1; ---
                                                                                                                                                                                                                                                                       Gribanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Dryg Gusev A.A., Balyshev V.M., Zhesterev V.I., Vishnjakov I.F., "Phylogenetic analysis of Newcastle disease virus of Russia.", Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR000665; Pfam; PF00423; HN; 1.
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STRAIN=zj/2000;
Zhou J.Y., Ye J.X., Chen Q.X., Wang J.Y., Chen Submitted (JUL-2002) to the EMBL/GenBank/DDBJ d EMBL; AY135171; AAN08047.1; -.

SEQUENCE 577 AA; 63236 MW; 5EBC1A979387AE3A
                                                                                                                                                                                                      Q8BA53 PRELIMINARY; PRT; 577 AA.
Q8BA53;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hemagglutinin-neuraminidase.
Newcastle disease virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI TaxID=11176;
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                                           ; Score 2897; DE ; Pred. No. 3.8e- 9; Mismatches
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Q83840-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-JUN-2001 (TrEMBLrel. 17, L
Hemaglutinin-neuraminidase.
                                                                                                                              SEQUENCE FROM N.A.

STRAIN-vaccine 4;

MEDLINE=96414821; PubMed=8817822;

Seal B.S., King D.J., Bennett J.D.;

"Characterization of Newcastle disease virus vaccines by biological properties and sequence analysis of the hemagglutinin-neuraminidase protein gene.";

Vaccine 14:761-766(1996).

EMBL; U37190; AAC55044.1; -.

EMBL; U37190; AAC55044.1; -.

InterPro; IPR000665; Hem-neuramndse.

Pfam; pF00423; HN; 1.

SEQUENCE 577 AA; 63231 MW; ACC95422982C7878 CRC64;
                                                                                                                                                                                                                                                                                                                Newcastle disease virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI_TaxID=11176;
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llarity 95.7%;
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Vaccine 14:761-766(1996).
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Valctine 14:761-766(1996).

EMBL; U37191; An255045.1; -.

InterPro; IPR000665; Hem-neuramndse.

InterPro; IPR000665; Hem-neuramndse.

Pfam; PF00423; HN; 1.

Score 2887; DB 12; Leng
2.5e-228;
Ind
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STRAIN-vaccine 5;

MEDLINE-96414821; PubMed-8817822;

Seal B.S., King D.J., Bennett J.D.;

Seal B.S., King D.J., Bennett J.D.;

"Characterization of Newcastle disease virus vaccines by biological properties and sequence analysis of the hemagglutinin-neuraminidase
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hemaglutinin-neuraminidase.
Newcastle disease virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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Pred. No. 2.5e-228;
lO; Mismatches 14;
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01-NOV-1999
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Pfam; PF00423; HN; 1.
Glycosidase; Hydrolase.
SEQUENCE 577 AA; 63347 MW; 56734
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Sagrera A., Villar E.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ
EMBL; AF098289; AAD28331.1; -.
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in-neuraminidase (EC 3.2.
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Pred. No. 3.1e-228;
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ae; Rubulavirus.
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Matches 550; Conservative
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Q89712;
01-NOV-1996 (TrEMBLrel. (
01-NOV-1996 (TrEMBLrel. (
01-JUN-2001 (TrEMBLrel. 1)
                                                                                                                                                                                                                              Seal B.S., King D.J., Bennett J.D.;

"Characterization of Newcastle disease virus vaccines by biological properties and sequence analysis of the hemagglutinin-neuraminidase protein gene.";

Vaccine 14:761-766(1996).

EMBL; U37192, AAC55046.1; -.

EMBL; U37189, AAC55043.1; -.
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STRAIN=VACCINE 6;
MEDLINE=96414821; PubMed=8817822;
                                                                                                                                                                                                                                                                                                                                                                                                                 Newcastle disease virus.
Viruses; seRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI_TaxID=11176;
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MEDLINE=9641821; PubMed=8817822;

Seal B.S., King D.J., Bennett J.D.;

"Characterization of Newcastle disease virus vaccines by biological properties and sequence analysis of the hemagglutinin-neuraminidase protein gene.";

Vaccine 14:761-766(1996).

EMBL; U37188; AAC55042.1; -

InterPro; IPR000665; Hem-neuramndse.

Pfam; PF00423; HN; 1.

SEQUENCE 577 AA; 63174 MW; E3241EDB48B4CB33 CRC64;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
Hemaglutinin-neuraminidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Newcastle disease virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales.
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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δ	241	SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYP 300	0
ъ	241	SATPLGCDMLCSKVTETEEEDYNSAVPTRMVHGRLGFDGQYHEKDLDVTTLFGDWVANYP 300	Ō
Ϋ́	301	GVGGGSFIDGRVWFSVYGGLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYK 360	0
ъ	301	GVGGGSFIDSRVWFSAYGGLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYK 360	0
ν	361	PGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY 420	0
ъ	361	PGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY 420	0
Ϋ́C	421	FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR 480	0
ъ	421	FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNPCVTGVYTDPYPLIFYR 480	0
Ϋ́	481	NHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAVTTSTCFKVVKTNKT 540	0
90	481	NHTLRGVFGTMLDGVQARLNPTSAVFDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKT 540	0
γ	541	YCLSIAEISNTLFGEFRIVPLLVEILKNDGVREARSG 577	
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; APPLICANT: Bingham, Richard W.;Chambers, Philip;Emmerson,
;T.;Millar, Neil S.
;TITLE OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES
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FILING DATE: 17-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 885,765
FILING DATE: 15-JUL-1986
SEQ ID NO:3:
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CURRENT APPLICATION DATA:
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ALIGNMENTS

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Query Match
Best Local Simi
Matches 572;
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                                                                                                                                                                               MDRAVSQVALENDEREAKNTWRLIFRIAILLLTVVTLATSVASLVYSMGASTPSDLVGIP
                                                                                                                               GVGGGSFIDGRVWFSVYGGLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYK
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FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR 480
                                                       PGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY
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                                                                                                           GVGGGSFIDGRVWFSVYGGLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYK
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                                PGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY
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Pred. No. 3.
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Best Local Similarity
Matches 559; Conserv
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Patent No. 5
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APPLICANT: Cochran Ph.D., Mark
APPLICANT: Junker M.S., David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: AMINO ACID
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
7-820-154A-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Recombinant Swinepox Virus NUMBER OF SEQUENCES: 40
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STREET: 30 Rockefeller Plaza
CITY: New York
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FILING DATE: 19920113
CLASSIFICATION: 424
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SATPLGCDMLCSKVTETEBEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDMVANYP
                                                                            SATHYCYTHNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSV 240
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96.9%;
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Pred. No. 5.1e-295;
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                                                                                                              Matches
                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/663
FILING DATE: June 13, 1996
CLASSIFEICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
                                                                                                                                                                                                                                                                                          TELEX: 422523
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
LENGTH: 577 amino acid
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TITLE OF INVENTION: Recombinant Herpesvirus of
TITLE OF INVENTION: and Uses Thereof
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APPLICANT: Macdonald, Rich
                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                             TELEFAX:
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   TRISRAEEKITSALGSNQDVVDRIYKQVALESPLALLNTETTIMNAITSLSYQINGAANN 120
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Pred. No. 5.1e-295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5869312
GENERAL INFORMATION:
GENERAL OCCHRAN Ph.D., Mark D
APPLICANT: Junker M.S., David B
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30, Application US/08097554A Patent No. 5869312
                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,554A
FILING DATE: July 22, 1993
CLASSIFICATION: 435
                                                  TELEX: 422523
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
   MOLECULE TYPE:
                   TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                   TELEPHONE:
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Best Local Similarity
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                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 APPLICANT: Cochran Ph. D., Mark D
APPLICANT: Macdonald Ph. D., Richard D
TITLE OF INVENTION: Recombinant Herpesvirus
TITLE OF INVENTION: and Uses Thereof
                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
APPLICATION NUMBER: US/08/023,610 FILING DATE: February 26, 1993 CLASSIFICATION: 435
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                                                                                                                                                                                  COUNTRY: USA
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Pred. No. 5.1e-295;
8; Mismatches 10;
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PATENT NO. 5961982
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
TITLE OF INVENTION: HVT-050 and Uses Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
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               ADDRESSEE: John P. White
STREET: 1185 Avenue of the
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LENGTH: 577 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-288-065A-11
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RESULT 7
US-08-362-240A-11
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Best Local Similarity 96.9%;
Matches 559; Conservative
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/288,065A
FILING DATE: Aug-09-94
CLASSIFICATION: 435
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NAME: White, John P
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEPAX: (212)391-0526
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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Pred. No. 5.1e-295;
8; Mismatches 10;
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Length 577; Indels

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TELEX: 42523
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION UMBER: US/08/362,240A
FILING DATE: Dec-22-94
CLASSIFICATION: 435
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APPLICANT: Junker, David
APPLICANT: Wild, Martha A
TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
NUMBER OF SEQUENCES: 60
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REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
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ADDRESSEE: John P. White
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                        GVGGGSFIDSRVWFSVYGGLKPNTPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYK 360
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96.9%;
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Pred. No. 5.1e-295;
8; Mismatches 10;
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US-08-480-640A-30
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                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 391-052
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 291-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,640A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
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                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                   SATHYCYTHNVILSGCRDHSHSHQYLALGVLRTSATGRVFFSTLRSINLDDTQNRKSCSV
                                                                                              SATHYCYTHNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSV
                                                                                                                                                          SGWGAPIHDPDFIGGIGKELIVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDM
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                      SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYP
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SATPLGCDMLCSKATETEEEDYNSAVPTRMVHGRLGFDGQYHEKDLDVTTLFGDWVANYP
                                                                                                                                         SGWGAPIHDPDYIGGIGKELIVDDASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDM
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Pred. No. 5.1e-295;
8; Mismatches 10;
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GENERAL INFORMATION:
                                                                                                                                                       Query Match
Best Local Similarity
Matches 559; Conserv
                                                                                                                                                                                                                                                                                                 TELEX: 422523
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,802
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                         NAME: White, John PRITELECOMMUNICATION: TELECHMONE: (212)977-9550
TELEPHAX: (212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 188
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ADDRESSEE: John P. W
                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
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o. 6127163
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                                                                                                         1 MDRAVSQVALENDEREAKNTWRLIFRIAILLLTVVTLATSVASLVYSMGASTPSDLVGIP
                                    TRISRAEEKITSALGSNQDVVDRIYKQVALESPLALLNTETTIMNAITSLSYQINGAANN 120
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                  TRISRAEEKITSTLGSNQDVVDRIYKQVALESPLALLNTETTIMNAITSLSYQINGAANN
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                                                                                                                                                            Conservative
                                                                                                                                                                             97.48;
96.98;
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                                                                                                                                                          8; Mismatches
                                                                                                                                                          Score 2920; DB 3;
Pred. No. 5.1e-295;
8; Mismatches 10;
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US-08-804-372A-9
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                                                 TELEPHONE: (212) 278-041
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 'SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cochran, Mark u.
APPLICANT: Wild, Martha A.
APPLICANT: Winslow, Barbara J.
                                                                                                                                                                       CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                       REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                 SOPTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/804,372A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
 MOLECULE TYPE:
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                  TYPE: amino acid TOPOLOGY: linear
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Y: USA
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85 Avenue of the Americas
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                                                                                                                                                                                                                                                      Patent No. 6251403

Patent No. 6251403

GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Counker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
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Best Local
          COUNTRY: USA
ZIP: 1036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Veri
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,237A
FILING DATE: 07-UN-1995
CLASSIFICATION: 424
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                             STREET: 1185 Ave
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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96.9%;
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Pred. No. 5.1e-295;
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US-08-375-992A-30
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US-08-488-237A-30
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH:: 577 antino acids
                                                                                                                                                                          Sequence 30, Application US/08375992A
Patent No. 6328975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.4%;
Best Local Similarity 96.9%;
Matches 559; Conservative
                                                                                                                                                            GENERAL INFORMATION:
                                                                                        APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant
NUMBER OF SEQUENCES: 220
                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. W
        CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                             STREET:
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REGISTRATION NUMBER:
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                                             1185 Avenue of
                                                           John P. White
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Pred. No. 5.1e-295;
8; Mismatches 10;
                                                                                                           Swinepox Virus
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ATTORNEY AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-375-992A-30
                              RESULT 13
US-08-472-679H-30
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Sequence 30, Patent No. 64
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Best Local Similarity 96.9
Matches 559; Conservative
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR COMPATION
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/375,992A
FILING DATE: Herewith
CLASSIFICATION: 424
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6497882
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                                                                                                                        YCLSIAEISNTLFGEFRIVPLLVEILKNDGVREARSG 577
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                                                                                                                                                                           NHTLRGVFGTMLDGEQARLNPASAVFDSTSRSRITRVSSSSIKAAYTTSTCFKVVKTNKT
                                                                                                                                                                                                                                                                   FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR
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96.9%;
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Pred. No. 5.1e-295;
8; Mismatches 10;
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Best Local S
Matches 559
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TELECOMMUNICATION IMPORMATION:
TELEPHONE: (908) 298-2135
TELEPAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/472,679H
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Salkeld, Pamela G.
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ADDRESSEE: Pamela G. Salkeld
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Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
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COUNTRY: USA
NHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKT
                                                                                                                                                                                           GVGGGSFIDGRVWFSVYGGLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYK 360
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                                                      FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR 480
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Pred. No. 5.1e-295;
8; Mismatches 10;
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PCT-US93-00324-30
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: White, John P
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (212)977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/003: FILING DATE: 19930113
CLASSIFICATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: . IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Junker M.S., David E
                                                                                                                                                                                                                                                                                                                                                                                                       Local
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TYPE: AMINO ACID
TOPOLOGY: linear
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STATE: New York
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 GVGGGSFIDSRVWFSVYGGLKPNTPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYK 360
                     GVGGGSFIDGRVWFSVYGGLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYK 360
                                                              SATPLGCDMLCSKATETEEEDYNSAVPTRMVHGRLGFDGQYHEKDLDVTTLFGDWVANYP 300
                                                                                  SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYP 300
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30 Rockefeller Plaza
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96.9%;
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Pred. No. 5.1e-295;
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PCT-US95-10245-11
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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Pred. No. 5.1e-295;
8; Mismatches 10;
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anuary 2, 2004, 16:17:21	completed: January	Search comple	Se
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YCLSIABISNTLFGEFRIVPLLVEILKNDGVREARSG 577		541	δ
NHTLRGVFGTMLDGEQARLNPASAVFDSTSRSRITRVSSSSIKAAYTTSTCFKVVKTNKT		481	밁
NHTLRGVFGTMLDSEQARLNFASAVFDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKT		481	δ
FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR		421	밁
FSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYR		421	ð
PGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY		361	밁
PGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSY		361	S
GVGGGSFIDSRVWFSVYGGLKPNTPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYK		301	В
GVGGGSFIDGRVWFSVYGGLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYK		301	S
SATPLGCDMLCSKATETEEEDYNSAVPTRMVHGRLGFDGQYHEKDLDVTTLFGDWVANYP		241	뮹
SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYP		241	Ş
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Result
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( 'Ggn2 6 / ptodata/1 / pubpaa/USO7 PUBCOMB.pep:*

( 'Ggn2 6 / ptodata/1 / pubpaa/PCT NEW PUB.pep:*

( 'Ggn2 6 / ptodata/1 / pubpaa/USO6 NEW PUB.pep:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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9 US-09-915-515A-1

12 US-10-226-629A-17

9 US-09-841-132-394

13 US-09-841-132-394

14 US-09-975-719-405

12 US-10-172-502-4

15 US-10-142-515-11

15 US-10-243-243A-8

15 US-09-815-242-12713

12 US-09-915-242-12713

12 US-09-965-738-146

12 US-09-965-738-162

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17 US-09-965-738-162

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                Sequence 1, Appli
Sequence 17, Appl
Sequence 394, App
Sequence 394, App
Sequence 4, Appli
Sequence 11, Appl
Sequence 11, Appli
Sequence 12713, Appli
Sequence 12713, Appli
Sequence 162, Appli
Sequence 163, Appli
Sequence 1707, Appli
Sequence 1733, Appli
Sequence 1733, Appli
Sequence 1733, Appli
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e 22068 e 12, # e 3553, e 8553, e 8553, 594, #	3291, 8291, 118, p 118, p 326, p 1198, p	5176 5177 46, 2225 2227 1789	2, Api 16732, 2, Api 2, Api 2, Api 2, Api 6698, 48, Ai	Sequence 93, Appl Sequence 136, App Sequence 136, Appl Sequence 70, Appl Sequence 22177, A

ALIGNMENTS

RESULT 1 US-09-915-515A-1

8 8	망	Q	Дb	Ş	Matches	Query Match	; ORGANISM: Ne US-09-915-515A-1	; TYPE	; SEQ ID NO 1	; CURRE	; CURRE	; FILE	; TITLE	; TITLE OF I	APPLICANT	; APPLICANT	; APPLICANT	; APPLICANT:	; GENERA	; Patent	Seguen
121 SGWGAPIHDPDFIGGIGKELIVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDM 180		61 TRISRAEBKITSALGSNQDVVDRIYKQVALESPLALLNTETTIMNAITSLSYQINGAANN 120	1 MDRAVSQVALENDEREAKNTWRLIFRIAILLLTVVTLATSVASLVYSMGASTPSDLVGIP 60	1 MDRAVSQVALENDEREAKNTWRLIFRIAILLLTVVTLATSVASLVYSMGASTPSDLVGIP 60	Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%; Score 2998	ORGANISM: Newcastle Disease Virus (Kansas Strain) 9-915-515A-1		NO 1	NUMBER OF SEQ ID NOS: 1	z	3	INVENTION: and Uses Thereof	OF INVENTION: Three Dimensional Structure of Paramyxovirus Hemaqqlutinin-Neurami	Babu, Y.	: Takimoto	CANT: Portner, Allen	Taylor, G	GENERAL INFORMATION:	Patent No. US2020081572A1	: Sequence 1. Application US/09915515A

Sequence

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APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226,629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
PRIOR PILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 736
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/10226629A Publication No. US20030166504A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 Matches 155;
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Best Local Similarity
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                                                                                                                                                                                                             92 --RQEVISRTINIQSSVQSGIPILLNKQSRDLTQLIEKSCNRQELAQICENTIAIHHADG 149
                                                                                                                                                                                                                                                                                              32 RIHIWLLIATTMHTVLSFIIMILCIDLIIKQDTCMKTNIMTVSSMNBSÄKTIKETITELI 91
                                                                                                                                                                                                                                                                                                                                     26 RIAILLITVVTLATSVA------SLVYSMGASTPSDLVGIPTRISRA---EEKITSAL
                                                                                                                                                                                                                                                    GSNQDVVDR-IYKQVALESPL-ALLNTETTIMNAITSLSYQINGAANNSGWGAPIHDPDF 132
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  SCSVSATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRLGFDG-----QYHEKDLDVTTL 291
                                         SLSIGDAIYAYSSNLITQGCADIGKSYQVLQLGYISLNSDMYPDLNPVISHTYDINDNRK
                                                                                SFDMSATHYCYTHNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRK 236
                                                                                                                                                                   IG-----TTGSGCTRIP 176
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                                                                                                                            ISPLDPHDFWRCPVGEPLLSNN------PNISLLPGPSLLSGSTTISGCVRLP 196
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                                                                                                                                                                                                                                                                                                                                                                              14.9%; Score 446; DB 12; Length 575;
27.5%; Pred. No. 5.2e-35;
tive 92; Mismatches 237; Indels 8
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469CB
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 395
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 4.8%; Score 145; DB 9; Local Similarity 18.8%; Pred. No. 0.00028;
                     733
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                 TKNAAFSNISSVTFDONTSSENGGALLTOKAADKTDCSFTYITNVNITNNTATGNGGGIA
                                                                                                                                                                                                                                                                        AKGGALYSTEGLTVSGITSILSFENNECQNQGGGAYVTKTFQCSDSHRLQFTSNKAADEG
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                                                             ----FSTLRSISLDDTQNRKSCSVSATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRL
                                                                                                                                             GCTRIPSFDMSATHYCYTHNVILSGCRDHSHSH------QYLALGVLRTTATGRIF 220
                                                                                                                                                                                                                            GGI--GKELIVDNASDVTSFYPSAFQEH------
                                                                                                                                                                                                                                                                                                                                                             GITLSDLVEVRFSKNKTGNYSAPITKAASNTAPVVS---SSTTAASPAVPAAAAAPVTNA 565
                                                                                                                                                                                                                                                                                                                                                                                                                                              AVGQVTLEDIANLKMTNNTCKGEGGAIYTKKALTINNGAILTTFSGNTSTDNGGAIFAVG
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                                                                                                                                                                                       GGLYCGDDVTLTNLTGKTLFQENSSEKHGGGLSLASGKSLTMTSLESFCLNANTAKENGG
                                                                                                                                                                                                                                                                                                                   ----ALLNTETTIMNAITSLSYQINGAANNSGWGAPI-----HDPDFI------ 133
                                                                                                                                                                                                                                                                                                                                                                                                  ASTPSDLVGI----PTRISRAEEKITSALGSNQDVVDRIYKQVALESPL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VYTDAYPL----SPDAVNVATTTLYANTSRVNP-TIMYSSTSKIINMLRLKNGQLEAAYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09841132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae
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                                                                                                      ENIVLIFTYTPTPNEPAPVQQPVYGEALVTGNTATKSGGGIY
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APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
ITITE OF INVENTION: COMPOSITIONS AND METHODS FOR
ITITE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFE
FILE REFERENCE: 210121.469CB
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 394
LENGTH: 1723
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-841-132-394
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Best Local
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4.8%; Score 144; DB 9; Length 1723;
Local Similarity 18.8%; Pred. No. 0.00035;
hes 141; Conservative 88; Mismatches 284; Indels 23
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     G-ANVP----
                                                                                                                                                                                                                  AKGGALYSTEGLTVSGITSILSFENNECQNQGGGAYVTKTFQCSDSHRLQFTSNKAADEG 625
                                                                                                                                                                                                                                                                                                                           GITLSDLVEVRFSKNKTGNYSAPITKAASNTAPVVS---SSTTAASPAVPAAAAAPVTNA 565
                                                                                                                                                                                                                                                                                                                                                                                ASTPSDLVGI----PTRISRAEEKITSALGSNQDVVDRIYKQVALESPL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVSQVALEN--DEREAKNTWR-------LIFRIAILLLTVVTLATSVASLVYSMG 49
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                                                     GCTRIPSFDMSATHYCYTHNVILSGCRDHSHSH------
                                                                                                          GGLYCGDDVTLTNLTGKTLFQENSSEKHGGGLSLASGKSLTMTSLESFCLNANTÁKENGG 685
                                                                                                                                                             GGI -- GKELIVDNASDVTSFYPSAFQEH------
                                                                                                                                                                                                                                                                        ----ALLNTETTIMNAITSLSYQINGAANNSGWGAPI-----HDPDFI----- 133
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  -- ENIVLTFTYTPTPNEPAPVQQPVYGEALVTGNTATKSGGGIY 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 236;
                                                  -QYLALGVLRTTATGRIF 220
                                                                                                                                                             -----LNFIPAPTTGS 170
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Publication No. US20030023349A1

GENERAL INFORMATION:

APPLICANT: Ausubel, Frederick M.

APPLICANT: Rahme, Laurence G.

TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID

TITLE OF INVENTION: SEQUENCES AND USES THEREOF

FILE REFERENCE: 00786/361003

CURRENT APPLICATION NUMBER: US/09/975,719

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 09/199,637

PRIOR APPLICATION NUMBER: US 09/199,637

PRIOR PILING DATE: 1998-11-25

PRIOR PILING DATE: 1998-11-25

PRIOR FILING DATE: 1997-11-25

NUMBER OF SEQ ID NOS: 437

SOFTMARE: FastSEQ for Windows Version 4.0
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US-09-975-719-405
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                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542 CLSIAEISNTLFGEFRIVPLLVEILKNDG 570
150 DYPVPRFTAAWQDGYAQGSTTNLSNNYRPQWGTGWLGCIDSSCNTGRAYYYTYKVSASCP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                935 LFSNNSAATKKTSTTKQIAGGAIFSAAVTIENNSQPIIFLNNSAKSEATTAATAGNKDSC 994
                                                  151 FYP----SAFQEHL-----NFIPAPTTG-----SGC-----TRIP 176
                                                                                                                                                          106 AITSL-----SYQINGAANNSG------WGAPIHDPDFIGGIGKELIVDNASDVTS 150
                                                                                                                                                                                                                33 IPTDWSQRMIHQITRAGKSLLAA-GCTLSILFASDSYAATALNVSQQPLFL--TQGVAPN
                                                                                                        90 LLFTLDDSGSMAWAYVPDGISGNSGRAGRSSDYNALYYNPDYAYQVPKKLTLSGDQIIVS
                                                                                                                                                                                                                                                               59 IPT-----RISRAEEKITSALGSNQDVV--DRIYKQVAL---ESPLALLNTETTIMN
                                                                                                                                                                                                                                                                                                                             83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KASINNLGAAIYGNNETSDVTISLSAENG 1143
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                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                     4.0%; Score 119; DB 11; Length 1198;
21.3%; Pred. No. 0.06;
tive 53; Mismatches 112; Indels 142
                                                                                                                                                                                                                                                                                                                        Indels 142;
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US-10-172-502-4
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/172,502
CURRENT FILLIG DATE: 2002-06-17
CURRENT APPLICATION NUMBER: US 60/298,098
PRIOR FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FOSTER, Timothy et al.
TITLE OF INVENTION: CROSS-REACTIVE MONOCLONAL AND POLYCLONAL ANTIBODIES. .
FILE REFERENCE: P07263US01/BAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                        SMSDSVSTSGSTQQSQSVSTSKADSQSAS----TSTSGSIVVSTSASTS-----KST
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                                                                                                                                                                                                                                                                                                                               CYTHNVILSGCRDHSHS-----HQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSC
                                                                                                                                                                                                                                                                                                                                                                                                  PIHDPDFIGGIGKELIVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDMSATHY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVTNTVTGLPSGLSYD---SATNSIIGTPTKIGQSTVTVVSTDQANNKSTTTFTINVVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVVTLATSVAS-LVYSMGASTPSDLVGIPTRISRAEEKITSALGSNQ------DVVD-
   LSDSTSTSGSVSGSLSIAASQSVSTSTSDSMSTSEIVSDSIST----SGSLSASDSKSMS 1042
                                     -----PGRFGGKRIQQAILSIKVSTS-----LGEDPVLTVPPNTVTLMGAEGRILT
                                                                          TSNAISTSISESASTSDSISISNSIANSQSASTSKSDSQSTSISLSTSDSKSMSTSES
                                                                                                                                              NSSSTEKSESLSTSTSDSLRTSTSLSDSLSMSTSGSLSKSQSLSTSISGSSSTSASLSDS
                                                                                                                                                                                                                     SVS---LSDSVSASKSLSTSESNSVSSSTSTSLVNSQSVSSSM--SDSASKSTSLSDSIS
                                                                                                                                                                                                                                                        SVSATPLGCDMLCSKVTETEEED-YNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                        TAPTVTPIGDQSSEVYSPI---SPIKIATQDNSGNAVTNTVTGLPSGLTFDSTNNTISGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----RIYKQVALESPLALL---NTETTIMNAITSLSYQIN-GAANNSGWGA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.9%;
                                                                                                            ----SPSDTVQEGKYVIYKRYNDTC-PDEQDYQIRMAKSSYK-----
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3%; Pred. No. 0.34;
82; Mismatches 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSFIDGRVWFSVYGGLKENSPSDTVQEGK-YVIYKRY----
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                                                                                                                                                                                   ----YPGVGGGSFIDGRVWFS
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FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)...(5877)
OTHER INFORMATION: Amino
US-10-142-515-11
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US-10-142-515-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 5877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SLOAN-KEITERING INSTITUTE FOR CANCER RESEARCH APPLICANT: Lloyd, Kenneth O. APPLICANT: Yin, Beatrice W.T.
TITLE OF INVENTION: Nucleic Acid Sequence Encoding Ovaria
FILE REFERENCE: 649-A-US
CURRENT APPLICATION NUMBER: US/10/142,515
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/290,480
PRIOR FILING DATE: 2001-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human Being
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                                      1186 SSGITRIEIESMSSLTPGLRETRTSQDITSSTETSTVLYKMPSGATPEVSRTEVMPSSRT 1245
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                                                                                                                                                         MAHGRLGFDGQYHEKDLDVTTLFEDWVANYPG-----VGGGSFIDGRVWFSVYG
                                                                                                                                                                                                VPVTSLFTSIMMKATDMLDASLEPETTSAPNMNITSDESLAASKAT-TETEAIHVFENTA 1138
                                                                                                                                                                                                                                                                                                                   YCYTHNVILS----GCRDHS------HSHQYLALGVLRTTATG-----
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  YKPGRFGGKRIQQAILSIKVS----TSLGEDPVL----
                                                                                                                                                                                                                                   ----RIFFSTLRSIS--LDDTQNRKSCSVSATPLGCD--MLCSKVTETEBEDYNSAVPTL 269
                                                                                                                                                                                                                                                                              QRFPRSVVTTPMSRGPEDVSWPSPLSVEKNSPPSSLVSSSSVTSPSPLYSTPSGSSHSSP 1079
                                                                                                                                                                                                                                                                                                                                                                                               KELIVDNASDVTSFYPSAFQEHLNFIPAPTTG-SGCTRIPSFDM------SATH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                        EETSSATEKSTVLSSVPTGATTEVSRTEAISSSRTSIPGPAQST-------MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDVVDRIYKQVALESPLALLNTETTIMNAITSLSYQINGAANNSGWGAPIHDPDFIGGIG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGVYTDPYPLIFYRNHTLRGVFGTMLDSEQARLNPASAVFDSTSRSR-----ITRV 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGTSHFLYORGSSYFSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCV 466
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                                                                                                                    -VETTSATEELYSSSPGFSEPTKVISPVVTSSSIRDNMVSTTMPG
                                                                           GLKPNSPSDTV---QEGKYVIYKRYNDTCPDEQDYQIRMAKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96;
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Pred. No. 2.6;
96; Mismatches
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QY 218RIFFSTLRSISLDDTQNRKSCSVSATPLGCDMLCSKVTETEEEDYNSAVPTL 269	96; Mis	T APPLICATION NUMBER: US/10/243,243A T FILING DATE: 2002-09-19 APPLICATION NUMBER: US 10/142,515 FILING DATE: 2002-05-09 APPLICATION NUMBER: PCT/US02/14768 FILING DATE: 2002-05-09 APPLICATION NUMBER: US 60/290,480 FILING DATE: 2001-05-11 OF SEQ ID NOS: 10 SECY: HOMO sapiens RE: MISC FEATURE ION: (1):(5935) INFORMATION: Amino acid sequence of MUC16B -243A-8 atch 3.8%; Score 114; DB 15; Length 5935; atch satch 3.8%; Score 114; DB 15; Length 5935;		Db 1246 SIPGPAQSTMSLDISDEVVIRLSTSPINTESAEITITTQTGYSLATSQVTLPLG 1299 Qy 394 T-VTLMGAEGRILTVGTSHFLYQRGSSYFSPALLYPMTVS 432
Query Match 3.8%; Score 112.5; DB 9; Length 2344; Best Local Similarity 18.9%; Pred. No. 0.8; Matches 125; Conservative 89; Mismatches 251; Indels 195; Gaps 24;	PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: 60/242,578 PRIOR APPLICATION NUMBER: 60/253,625 PRIOR APPLICATION NUMBER: 60/253,625 PRIOR PILLING DATE: 2000-11-27 PRIOR APPLICATION NUMBER: 60/257,931 PRIOR APPLICATION NUMBER: 60/257,931 PRIOR PILLING DATE: 2000-12-22 PRIOR PILLING DATE: 2000-12-26 PRIOR PILLING DATE: 2001-02-16 NUMBER OF SEQ ID NOS: 14110 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12713 LENGTH: 2344 TYPE: PRI ORGANISM: Staphylococcus aureus US-09-815-242-12713		Qy 477 IFVENHTLEGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSS 521	Qy 270 MAHGRIGFDQQYHEKDLDVTTIFEDWVANYPGVGGGSFIDGRVWFSVYG 318

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; TYPE: PRT; ORGANISM: Homo sapie; ORGANISM: Homo sapie; FBATURE; NAME/KEY: VARIANT; LOCATION: (1)..(9799; OTHER INFORMATION: AUS-09-965-738-146
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US-09-965-738-146
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                                                                                                                                                                                       APPLICANT: O'Brien, Timothy
TITLE OF INVENTION: Repeat Sequences of the CA125 Gene and Their Use:
TITLE OF INVENTION: Therapeutic Interventions
FILE REFERENCE: 40715-258841
CURRENT APPLICATION NUMBER: US/09/965,738
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/284,175
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 306
SOFTWARE: PatentIn version 3.0
SEQ ID NO 146
SEQ ID NO 146
   Query Match
Best Local Similarity
Matches 117; Conserve
                                                                                                                                                                                                                                                                                                                                                                             Publication No. US201
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 146, Application US/09965738 Publication No. US20030143667A1
                                                                                                                                                                                  LENGTH: 9799
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 3.7%; Scilarity 19.8%; Pr
Conservative 76;
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Score 111; DB 12;
Pred. No. 12;
6; Mismatches 198;
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                                 Length 9799;
   Indels 200;
   Gaps
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   28;
                                                                                                                                                                                                                                           TITLE OF INVENTION: Repeat Sequences of the CA125 Ger
TITLE OF INVENTION: Therapeutic Interventions
FILE REFERENCE: 40715-258841
CURRENT APPLICATION NUMBER: US/99/965,738
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/284,175
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 306
SOFTWARE: Patentin version 3.0
SEQ ID NO 162
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 162, Application US/09965738
Publication No. US2003014367A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy
                                                Best Local Similarity Matches 117; Conserv
                                                                                                                              TYPE: PRT
ORGANISM: Homo mapienm
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)..(11721)
OTHER INFORMATION: any x = a:
                                                                                                                                                                                                                                 ENGTH: 11721
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                                                            3.7%;
19.8%;
                                                                                                                                 any amino
                                               76;
                                                Score 111; DB 12;
Pred. No. 16;
6; Mismatches 198;
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31 LLTVVTLATSVASLVYSMGASTPSDLVGIPTRISRABEKITSALGS---NQDVVDRIYKQ 87
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                                                                                                                                                           Length 11721
                                                                                                 Indels 200;
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                                                                                          Gaps
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RESULT 12
US-09-738-626-3707
; Sequence 3707, Application US/09738626
; Publication US20020197605A1
                                          ; ORGANISM: Corynebacterium glutamicum US-09-738-626-3707
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                                                                                                SOFTWARE: PatentIn ver.
SEQ ID NO 3707
LENGTH: 1510
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    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                  NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3256 SGCRLTLLRPEKHEAATGVDTICTHRVDPIGPGLDRERLYWELSQLTNSITELGP----- 3310
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                                                                                                                                                                                                                                                                                                                                                                                                                                 OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                  IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                             , AKIO
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    3.7%;
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  Score 109.5;
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  DB 10;
Length 1510;
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RESULT 13
US-10-369-493-1535
US-10-369-493-1535, Application US/10369493
; Publication No. US20030233675A1
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TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1535
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                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SEQ ID NO 1535
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                                                                                                                                          Query Match 3.6%; Score 108; DB 12; Best Local Similarity 19.4%; Pred. No. 1.2; Matches 123; Conservative 79; Mismatches 227;
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 GIGKELIVDNAS-----
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                                               748 LVLSTVTTTVNGAATEYTTWC--PASSIAYTTSISYKTLVLTTEVCSHSECTPTVITSVT
89 ALESPLALLNTETTIMNAITSLSYQINGAANNSGWGAPIHDPDFIGGIGKELIVDNASDV 148
                                                                                             30 LLLTVVTLATSVASLVYSMGASTPSDLVGIPTRISRAEEKITSALGSNQDVVDRIYKQV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYPGVGGGSFIDGRVWFSVYGG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FNPETIFKLQHATRSGSYEIFKDYTRKV--DDQSTRLGTIRGLFEFSTDRKPISVSEVEP 865
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                                                                                                                                            227; Indels 206;
                                                                                                                                                                                       Length 1609;
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US-10-032-189-128
; Sequence 128, Application US/10032189
; Publication No.: US20030170630A1
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Tchernev, Velizar T
                                                             APPLICANT:
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T: Smithson, Glennda INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                              Casman, Stacie J
Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Bdinger, Shlomit R
Gunther, Erik
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Grosse, William M
Lepley, Denise M
                                                           Millet, Isabelle
Sciore, Paul
Ellerman, Karen
                    MacDougall, John R
Smithson, Glennda
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Vernet, Corine A.M
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Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                        Burgess, Catherine E
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; LOCATION: (3367)
; OTHER INFORMATION:
US-10-032-189-128
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR FILING DATE: 2001-02-20
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PRIOR APPLICATION NUMBER: 60/277,826
PRIOR FILLING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
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Best Local Similarity 21.8%;
Matches 131; Conservative 65
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SEQ ID NO 128
LENGTH: 5636
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PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/311,754
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
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NAME/KEY: VARIANT
LOCATION: (3003)
OTHER INFORMATION: V
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: VARIANT
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                        SGPSPMIEIRNPLGKLIKKGFG--LHELLNIHNSAKVVNVKEPEAGMWTVKTSSSGRHSV 309
                                                         AVPTLMAH-----GRL---GFDGQYHE-----KDLDVTTLFED----WVANYPGVG----
                                                                                                                                                                                                                                                                                                  IGKELIVDNASDVTSFYPSAFQEHLNFI-----PAPTTGSGCTRIP-----SF---- 178
                                                                                                                                                                                                                                                                                                                                       FDVTGSMYDDLVQVIEGASKIL--ETSLKRPKRPL---FNFAL----VPFHDPE----
                                                                                                                                                                                                                                                                                                                                                                          QDVVDRIYKQV--ALESPLALLNTETTIMNAITSLSYQINGAANNSGWGAPIHDPDFIGG 135
                                                                                                  KKQVNEVLKWVEEAVQASKVHLLSTDHLEQ---
                                                                                                                                                                           TDARSKDYRLTHEVLQLIQQKQSQVVFVLTGDCDDRTHI-GYKVYEEIASTSSGQVFHLD
                                                                                                                                                                                                                  -DMSATHYCYTHNV------ILSG-CRDHSHSHQYLALGVLRTTATGRIFF--
                                                                                                                                                                                                                                                         IGPVTITTD-----PKKFQYELRELYVQGGGDCPEMSIGAIKIALEISLPGSFIYVF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wherein Xaa is
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                                                                                                                                       -----STLRSISLDDTQNRKSCSVSATPLGCDMLCSKVTETEEEDYNS 264
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; Pred. No. 9.5;
65; Mismatches 221;
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                                                                                                    -AVNTWRIPFDPSLKEVT-----VSL
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CURRENT APPLICATION NUMBER: US/10/120,801
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/285748
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 60/286068
PRIOR APPLICATION NUMBER: 60/286292
PRIOR APPLICATION NUMBER: 60/286292
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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US-10-120-801-72
; Sequence 72, Application US/10120801
; Publication No. US20030203843A1
; GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                           LENGTH: 5636
TYPE: PRT
ORGANISM: human
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APPLICANT: Edinger, Shlomit
APPLICANT: Smithson, Glennda
APPLICANT: Gunther, Erik
APPLICANT: Gunther, Erik
APPLICANT: Komuves, Laszlo
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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         LOCATION: (3041)
OTHER INFORMATION: Wherein Xaa is
                                                                           NAME/KEY: VARIANT
LOCATION: (3003)
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/285609
                                                                                                                                                                                                                                                                                         FILING DATE: 2001-09-14
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/
FILING DATE: 2001-05-03
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/322284
                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-05-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 ---GGSFIDGRVWFSVYGGLKP-----NSPSDTVQE-GKYVIYKRYNDTCPDEQDY--QI
                                                                                                                                                                                                                      Pacencin Ver.
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Spytek, Kimberly
Mehraban, Fuad
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Guo, Xiaojia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RMAKSSYK--PGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTS
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Malyankar, Uriel
Wasserman, Scott
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Padigaru, Muralidhara
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DS: 155
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Best Local (
                                    527 T
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512 T
                                                                      458 -----PFTLSFVRNGVTLGVDQYLKESASVSLDIAKVTLSDEGFYECIAVSSAGTGRAQ
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Similarity 21.8%;
                                                                                                                                            DYLFQRVSS-VSFSSIVPDAPKVTMPEKTP-----GYYLQPGQIPCSVDSLL-----
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                                                                                                                                                                                                                                                              RMAKSSYK--PGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTS
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                                                                                                        TGVYTDPYPLIFYRNHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAY 526
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512
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*; Pred. No. 9.5;

65; Mismatches 221;
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